

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 19, 2005, 20:07:21 ; Search time 179 Seconds  
(without alignments)  
1407.503 Million cell updates/sec

Title: US-10-756-778-8  
Perfect score: 2560  
Sequence: 1 IAEPPSTGVITOPRIINDNF.....KLSGKGEPALDISIFSPV 492

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2560	100.0	742	2	Q68UQ2
2	2473	96.6	723	2	Q9EVR2
3	244	9.5	829	2	Q6BE06
4	230	9.0	825	2	Q6BE09
5	228.5	8.9	1138	1	C7AA_BACTU
6	225.5	8.8	1138	1	C7AB_BACTU
7	223.5	8.7	1169	1	C9DA_BACTP
8	219.5	8.6	1138	1	C7AB_BACTK
9	214.5	8.4	810	2	Q6BE03
10	211.5	8.3	645	2	Q6BE03
11	210.5	8.2	1167	1	C1FA_BACTU
12	207.5	8.1	1169	1	C1FB_BACTM
13	207.5	8.1	1174	2	Q45749
14	207	8.1	660	2	Q6R0U6
15	200	7.8	1174	2	C1FA_BACTA
16	198	7.7	1154	2	Q6QAN9
17	197	7.7	1157	1	C9CA_BACTU
18	196	7.7	1157	1	C9CA_BACTO
19	194	7.6	659	1	C3BA_BACTO
20	193.5	7.6	682	1	C3BA_BACTH
21	193	7.5	1229	1	C1BB_BACTM
22	193	7.5	1233	1	C1BC_BACTM
23	190	7.4	686	2	Q75QO5
24	189.5	7.4	1220	1	C5AC_BACTU
25	187	7.3	1156	2	Q6GUL7
26	186	7.3	1118	2	Q9AM83
27	186	7.3	1155	1	C1AB_BACTK
28	186	7.3	1155	2	Q7BE98
29	185.5	7.2	719	1	C1ID_BACTU
30	185.5	7.2	793	2	Q6PYW7
31	184.5	7.2	793	2	Q6PYW7

32	184.5	7.2	1181	1	C1AB_BACTL	Q03748	bacillus th
33	184	7.2	649	1	C3CA_BACTK	Q45744	bacillus th
34	183.5	7.2	1289	1	C5AB_BACUD	Q45753	bacillus th
35	183	7.1	1118	2	Q9AM82	Q9AM82	bacillus th
36	183	7.1	1169	1	C8BA_BACTK	Q45705	bacillus th
37	183	7.1	1177	2	Q6EIX3	Q6EIX3	bacillus th
38	183	7.1	1231	2	Q6KNY2	Q6KNY2	bacillus th
39	183	7.1	1385	1	C5AA_BACUD	Q45760	bacillus th
40	182.5	7.1	1150	1	C9EA_BACTA	Q9ZNI9	bacillus th
41	182.5	7.1	1150	2	Q7IRP4	Q7IRP4	bacillus th
42	182	7.1	1231	1	C1BD_BACTZ	Q9ZAZ5	bacillus th
43	181.5	7.1	719	1	C1IB_BACTE	Q45709	bacillus th
44	180.5	7.1	1167	1	C1AA_BACTU	P56956	bacillus th
45	179	7.0	1155	2	Q93T21	Q93T21	bacillus th

ALIGNMENTS

RESULT 1					
068UQ2					
ID	068UQ2	PRELIMINARY;	PRT;	742 AA.	
AC	Q68UQ2;				
DT	25-OCT-2004 (TREMBLrel. 28, Created)				
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)				
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)				
DE	83-kDa crystal protein.				
GN	Name=Cry3Ia2;				
OS	Bacillus thuringiensis.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_Taxid=1428;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=M15;				
RA	Yung Y.-C., Cote J.-C.;				
RT	"83-KDa crystal protein gene from a novel autoagglutinable, non-ferrolyseable strain of Bacillus thuringiensis.";				
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY081052; AA87456.1; -				
DR	InterPro; IPR005639; endotoxin N.				
DR	InterPro; IPR008979; Gal bind like.				
DR	Pfam; PF03945; Endotoxin N; 1.				
DR	SEQUENCE 742 AA; 83104 MW; 40B1F7480B0CC134 CRC64;				
QY	Query Match	100.0%;	Score 2560;	DB 2;	Length 742;
	Best Local Similarity	100.0%;	Pred. No. 7.5e-182;		
	Matches 492;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	IAEPPSTGVITOPRIINDNF	KYAKLQFSTNSDLYPVLTPLRAQACV	MLLAKDA	60
DB	251	IAEPPSTGVITOPRIINDNF	KYAKLQFSTNSDLYPVLTPLRAQACV	MLLAKDA	310
QY	61	TTTSGGQIDISQQLNGYKALIRL	KYTTNDVNTYNOGLEKAKPLNTSDPREY	LAQ	120
DB	311	TTTSGGQIDISQQLNGYKALIRL	KYTTNDVNTYNOGLEKAKPLNTSDPREY	LAQ	370
QY	121	RPDISVRSNFKKVMKNNKVA	KYKRGAMGALSIALLPFTGPNY	POALKTVO	180
DB	371	RPDISVRSNFKKVMKNNKVA	KYKRGAMGALSIALLPFTGPNY	POALKTVO	430
QY	181	PVIGIPGIGTSQSGPTFGS	RRPVYKYDDIDALROLMBLYIOLKSA	YFMTYS	240
DB	431	PVIGIPGIGTSQSGPTFGS	RRPVYKYDDIDALROLMBLYIOLKSA	YFMTYS	490
QY	241	ATTVNDYIGKRGSTGAMH	MSDPSAITSALGAAGYAPNVVGV	YSHGSSYTK	300
DB	491	ATTVNDYIGKRGSTGAMH	MSDPSAITSALGAAGYAPNVVGV	YSHGSSYTK	550
QY	301	ANTNAVAPPEFKIPGYL	HSVAGLSKAPDADSVNFGFRPV	LTLEMANOL	1DTALQI 360
DB	551	ANTNAVAPPEFKIPGYL	HSVAGLSKAPDADSVNFGFRPV	LTLEMANOL	1DTALQI 610
QY	361	PATIGITDVVPAFORT	TEPINGDAILWESFSGPFTTV	VDSPQAKYII	IRIANNL 420

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Db      611 PAEIGITDVPAAGRTSEEPINGODAIRINESFTSGGFTTUDSPKOKKTIYRIANML 670
Qy      421 SASTVSLTYNNQTFPTDILNTSLDPNGVGNYSYTLVEGP1IEFSQGTNIFLGSQKGE 480
Db      671 SASTVSLTYNNQTFPTDILNTSLDPNGVGNYSYTLVEGP1IEFSQGTNIFLGSQKGE 720
Qy      481 FAIDSIIIFSPV 492
Db      731 FAIDSIIIFSPV 742

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## RESULT 2

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ID      Q9EVR2      PRELIMINARY;      PRT;      723 AA.
AC      Q9EVR2;
DT      01-MAR-2001 (T-EMBLrel. 16, Created)
DT      01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT      01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE      81-kDa leukemia toxin.
GN      Name=leuk81;
OS      Bacillus thuringiensis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1428;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=84-HS-1-11;
RX      MEDLINE=2034253; PubMed=10882663;
RA      Mizuki E., Park Y.S., Saitoh H., Yamashita S., Akao T., Higuchi K.,
RA      Ohba M.;
RT      "Parasporin, a human leukemic cell-recognizing parasporal protein of
RT      Bacillus thuringiensis.";
RL      Clin. Diagn. Lab. Immunol. 7:625-634(2000).
DR      EMBL; AB031065; BAB11757.1;
DR      InterPro; IPR005639; endotoxin N.
DR      InterPro; IPR008979; Gal_bind_Like.
DR      Pfam; PF03945; Endotoxin N.1.
SQ      SEQUENCE 723 AA; 81049 MW; 21F873E8286BF52 CRC64;

```

Query Match 96.6%; Score 2473; DB 2; Length 723;

Best Local Similarity 97.1%; Pred. No. 2.2e-175; Indels 0; Gaps 0;

Matches 477; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

```

Qy      1 IAEPPSTGVITQFRILNDFIKYIAKLQSTNQSDLOYVLTLPRAQACVMHMLKDA 60
Db      232 MAEPSTGVITQFRILNDFIKYIAKLQSTNQSDLOYVLTLPRAQACVMHMLKDA 291
Qy      61 TTSVWGQOIDSQOLNGYKAEILRLIKVTNDVNTYNNQGLEBKAKPLNYSDEEYLAQ 120
Db      232 TTSVWGQOIDSQOLNGYKAEILRLIKVTNDVNTYNNQGLEBKAKPLNYSDEEYLAQ 351
Qy      121 RPDISVLSNFKEMKMKVAKYKRGMAISLALPPTPGPNYPKOALKVVSROIFA 180
Db      352 RPDISVLSNFKEMKMKVAKYKRGMAISLALPPTPGPNYPKOALKVVSROIFA 411
Qy      181 PVIGIPGIGTSDSGPTFGSMRFVYKTYDQIDALQMLYLOPLKSAFYIYESDWKR 240
Db      412 PVIGIPGIGTSDSGPTFGSMRFVYKTYDQIDALQMLYLOPLKSAFYIYESDWKR 471
Qy      241 ATTYNDYIGKRGSGNTGAAMHMSDPSAIYTSALGAAGYAPNVVGRYHSGSYTKGAP 300
Db      472 ATTYNDYIGKRGSGNTGAAMHMSDPSAIYTSALGAAGYAPNVVGRYHSGSYTKGAP 531
Qy      301 AATNVAAPPEFYKPGYKLSVSYGLSKAPDAADSVWFGFRPYLNEANOLLTDALQI 360
Db      532 PNTNVAAPPEFYKPGYKLSVSYGLSKAPDAADSVWFGFRPYLNEANOLLTDALQI 591
Qy      361 PAEIGITDVPAAGRTSEEPINGODAIRINESFTSGGFTTUDSPKOKKTIYRIANML 420
Db      592 PAEIGITDVPAAGRTSEEPINGODAIRINESFTSGGFTTUDSPKOKKTIYRIANML 651
Qy      421 SASTVSLTYNNQTFPTDILNTSLDPNGVGNYSYTLVEGP1IEFSQGTNIFLGSQKGE 480

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Db      652 SASTVSLTYNNQTFPTDILNTSLDPNGVGNYSYTLVEGP1IEFSQGTNIFLGSQKGE 711
Qy      481 FAIDSIIIFSPV 491
Db      712 FAIDSIIIFSPV 722

```

## RESULT 3

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ID      Q6EB06      PRELIMINARY;      PRT;      829 AA.
AC      Q6EB06;
DT      25-OCT-2004 (T-EMBLrel. 28, Created)
DT      25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE      Cancer cell-killing Cry protein.
GN      Name=Cry41AD1;
OS      Bacillus thuringiensis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1428;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Al462;
RA      Yamashita S., Saitoh H., Katayama H., Akao T., Mizuki E., Park Y.,
RA      Ohba M., Ito A.;
RT      "Cell-killing toxin gene and other genes in 6,698bp DNA from Bacillus
RT      thuringiensis.";
RL      Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB116511; BAD35163.1;
DR      GO; GO:0005102; F:receptor binding; IEA.
DR      GO; GO:0006952; P:defense response; IEA.
DR      GO; GO:0009405; P:pathogenesis; IEA.
DR      InterPro; IPR001178; Endotoxin.
DR      InterPro; IPR005638; endotoxin C.
DR      InterPro; IPR005639; endotoxin N.
DR      InterPro; IPR008979; Gal_bind_Like.
DR      InterPro; IPR008979; RicinB_Like.
DR      InterPro; IPR000772; Ricin B lectin.
DR      Pfam; PF03944; Endotoxin C.1.
DR      Pfam; PF03945; Endotoxin M.1.
DR      Pfam; PF03945; Endotoxin N.1.
DR      Pfam; PF00652; Ricin B lectin. 3.
DR      SMART; SM00458; RICIN.1.
DR      PROSITE; PS05031; RICIN B LECTIN.1.
SQ      SEQUENCE 829 AA; 93841 MW; BBF1F3BEC05F97A3 CRC64;

```

Query Match 9.5%; Score 244; DB 2; Length 829;

Best Local Similarity 22.2%; Pred. No. 2.6e-09; Indels 152; Gaps 26;

Matches 128; Conservative 86; Mismatches 210; Indels 152; Gaps 26;

```

Qy      9 VITQFRILN---DNFIKIAKLQSTNQSDLOYVLTLPRAQACVMHMLKDAAT--S 63
Db      164 VITQFRILN---DNFIKIAKLQSTNQSDLOYVLTLPRAQACVMHMLKDAAT--S 214
Qy      64 VMGQOIDSQOLNGYKAEILRLIKVTNDVNTYNNQGLEBKAKPLNYSDEEY 116
Db      215 VMGQOIDSQOLNGYKAEILRLIKVTNDVNTYNNQGLEBKAKPLNYSDEEY 273
Qy      117 LQAGRPDISVLSNFKEMKMKVAKYKRGMAISLALPPTPGPNYPKOALKVVSROIFA 176
Db      274 LQAGRPDISVLSNFKEMKMKVAKYKRGMAISLALPPTPGPNYPKOALKVVSROIFA 333
Qy      177 QIPAVVIGIPGIGTSDSGPTFGSMRFVYKTYDQIDALQMLYLOPLKSAFYIYESDWKR 224
Db      334 QIPAVVIGIPGIGTSDSGPTFGSMRFVYKTYDQIDALQMLYLOPLKSAFYIYESDWKR 381
Qy      225 LKSAFYIYES-----DKVRAATYVND-YIGKRGSGNTGAA-----MH----- 260
Db      382 LKSAFYIYES-----DKVRAATYVND-YIGKRGSGNTGAA-----MH----- 441
Qy      261 -----MW-SSPSAIYTSALGAAGYAPNVVGRYHSGSYTKGAPAPATNVAAPPE 310
Db      442 -----MW-SSPSAIYTSALGAAGYAPNVVGRYHSGSYTKGAPAPATNVAAPPE 501

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 O | O IntelliGenetics  
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FastDB - Fast Pairwise Comparison of Sequences  
 Release 5.4

Results file seq8-seq18-232-723.res made by tport on Thu 27 Oct 105 16:23:23-PST.

Query sequence being compared: US-10-756-778-8 (1-492)  
 Number of sequences searched: 1  
 Number of scores above cutoff: 1

Results of the initial comparison of US-10-756-778-8 (1-492) with:  
 File: rook778.pep

```

100- -
N -
U -
M -
B -
E -
R -
O -
F 10-
S -
E 5-
O -
U -
N -
C -
E -
S 0-
SCORE 0 54 107 161 215 268 322 376 429 483
STDEV

```

## PARAMETERS

Similarity matrix PAM-150 K-tuple 1  
 Threshold level of sim. 16%  
 Mismatch penalty 1 Joining penalty 20  
 Gap penalty 5.00 Window size 492  
 Gap size penalty 0.05  
 Cutoff score 1  
 Randomization group 0

## SEARCH STATISTICS

Scores: Mean 483 Median 0 Standard Deviation 0.00  
 Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 492  
 Number of sequences searched: 1  
 Number of scores above cutoff: 1

The scores below are sorted by initial score.  
 Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Sig. Frame
1. SEQ18-232-723	Sequence 18, Application US/	492	483	484	0.00 0

1. US-10-756-778-8 (1-492)  
 SEQ18-232-723 Sequence 18, Application US/10756778

Initial Score = 483 Optimized Score = 484 Significance = 0.00  
 Residue Identity = 96% Matches = 477 Mismatches = 14  
 Gaps = 0 Conservative Substitutions = 1

X 10 20 30 40 50 60 70  
 IAEPPSGVITOPRIIINDNFIKTIKAKLQFSTNOSDLOYPVLTPLRAQACVMHMLLKDATTSSVGOQIDSO  
 MAEPPSGVITOPRIIINDNFIKTIKAKLQFSTNOSDLOYPVLTPLRAQACVMHMLLKDATTSSVGOQIDSO  
 X 10 20 30 40 50 60 70

QUNGKAEILRLIKVNTNDVNTTNOGLEBKAKPLNYSDEEYLQGRPDISVLRNFKEMKMKVAKYK  
 QUNGKAEILRLIKVNTNDVNTTNOGLEBKAKPLNYSDEEYLQGRPDISVLRNFKEMKMKVAKYK  
 80 90 100 110 120 130 140

RGMAASLSIALAEPPTGPNYPKQALKVQVOSROI FAPVIGIPGISTGDSGPFPGSRPVPVKTDOIDLAR  
 RGMAASLSIALAEPPTGPNYPKQALKVQVOSROI FAPVIGIPGISTGDSGPFPGSRPVPVKTDOIDLAR  
 150 160 170 180 190 200 210

LMELYIQLKSAFYIYESDWMKVATVNDYIGRGSGNTGAAHMMSSDPSATYTSALGAAGVAPNVGVRY  
 LMELYIQLKSAFYIYESDWMKVATVNDYIGRGSGNTGAAHMMSSDPSATYTSALGAAGVAPNVGVRY  
 220 230 240 250 260 270 280

SHGGSYTKGMAFPANTNAVAPPEFYPGKLSVSAVGLSKAPDAADSVMGFRVLLLENANQLLTDALOI  
 SHGGSYTKGMAFPANTNAVAPPEFYPGKLSVSAVGLSKAPDAADSVMGFRVLLLENANQLLTDALOI  
 290 300 310 320 330 340 350 360

PAEIGITDVVPAFGRTPEEPINGODAIRIWEFSFGFTYVDSPOKOKKIIRIANNUSASTVSLTYNNO  
 PAEIGITDVVPAFGRTPEEPINGODAIRIWEFSFGFTYVDSPOKOKKIIRIANNUSASTVSLTYNNO  
 370 380 390 400 410 420 430

TFPTDIINTSLDPNGVAGNGSYTLVVEGPIIEFSQTNIRKLSQKKEFALDSTIIEFSPV  
 TFPTDIINTSLDPNGVAGNGSYTLVVEGPIIEFSQTNIRKLSQKKEFALDSTIIEFSPV  
 440 450 460 470 480 490 X

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Maximum Match 100%

Listing first 45 summaries

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1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

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## SUMMARIES

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2	2473	96.6	723	Q68U02	Q68U02 bacillus th
3	244	9.5	829	Q68U06	Q68U06 bacillus th
4	230	9.0	825	Q68U09	Q68U09 bacillus th
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6	225.5	8.8	1138	Q68U09	Q68U09 bacillus th
7	223.5	8.7	1138	Q68U09	Q68U09 bacillus th
8	219.5	8.6	1138	Q68U09	Q68U09 bacillus th
9	214.5	8.4	645	Q68U03	Q68U03 bacillus th
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12	207.5	8.1	1169	Q68U03	Q68U03 bacillus th
13	207.5	8.1	1174	Q68U03	Q68U03 bacillus th
14	207	8.1	660	Q68U06	Q68U06 bacillus th
15	200	7.8	1174	Q68U06	Q68U06 bacillus th
16	198	7.7	1154	Q68U09	Q68U09 bacillus th
17	197	7.7	648	Q68U09	Q68U09 bacillus th
18	196	7.7	1157	Q68U09	Q68U09 bacillus th
19	194	7.6	659	Q68U09	Q68U09 bacillus th
20	193.5	7.6	682	Q68U09	Q68U09 bacillus th
21	193	7.5	1129	Q68U09	Q68U09 bacillus th
22	193	7.5	1233	Q68U09	Q68U09 bacillus th
23	190	7.4	686	Q68U09	Q68U09 bacillus th
24	189.5	7.4	1220	Q68U09	Q68U09 bacillus th
25	187	7.3	1156	Q68U09	Q68U09 bacillus th
26	186	7.3	1118	Q68U09	Q68U09 bacillus th
27	186	7.3	1155	Q68U09	Q68U09 bacillus th
28	186	7.3	1155	Q68U09	Q68U09 bacillus th
29	186	7.3	1155	Q68U09	Q68U09 bacillus th
30	185.5	7.2	719	Q68U09	Q68U09 bacillus th
31	184.5	7.2	793	Q68U09	Q68U09 bacillus th

32	184.5	7.2	1181	Q68U09	Q68U09 bacillus th
33	184	7.2	649	Q68U09	Q68U09 bacillus th
34	183.5	7.2	1289	Q68U09	Q68U09 bacillus th
35	183	7.1	1118	Q68U09	Q68U09 bacillus th
36	183	7.1	1169	Q68U09	Q68U09 bacillus th
37	183	7.1	1177	Q68U09	Q68U09 bacillus th
38	183	7.1	1231	Q68U09	Q68U09 bacillus th
39	183	7.1	1385	Q68U09	Q68U09 bacillus th
40	182.5	7.1	1150	Q68U09	Q68U09 bacillus th
41	182.5	7.1	1150	Q68U09	Q68U09 bacillus th
42	182	7.1	1231	Q68U09	Q68U09 bacillus th
43	181.5	7.1	719	Q68U09	Q68U09 bacillus th
44	180.5	7.1	1167	Q68U09	Q68U09 bacillus th
45	179	7.0	1155	Q68U09	Q68U09 bacillus th

## ALIGNMENTS

Query Match	Score	DB 2	Length	742
Beat Local Similarity	100.0%	Pred. No. 7.5e-182		
Matches 492	Conservative	0	Mismatches	0
Indels	0	Gaps	0	
1	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
2	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
3	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
4	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
5	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
6	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
7	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
8	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
9	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
10	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
11	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
12	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
13	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
14	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
15	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
16	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
17	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
18	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
19	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
20	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
21	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
22	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
23	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
24	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
25	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
26	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
27	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
28	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
29	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
30	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
31	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
32	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
33	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
34	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
35	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
36	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
37	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
38	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
39	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
40	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
41	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
42	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
43	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
44	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02
45	IAEPPSTGVITQFRLINDNF	Q68U02	Q68U02	Q68U02

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Db      611 PAEIGITDVPAFGRTBEEDINGODAIRIWEFTSGFTYVDSPOKQKXIIYRIANL 670
Qy      421 SASIVSLTYNNQTFPTDILNTSLDPNGVGNVGYTYLVEGPPIEFSGQINIFKLSQKGE 480
Db      671 SASIVSLTYNNQTFPTDILNTSLDPNGVGNVGYTYLVEGPPIEFSGQINIFKLSQKGE 730
Qy      481 FAIDSIIFSPV 492
Db      731 FAIDSIIFSPV 742

RESULT 2
Q6EVR2  PRELIMINARY; PRT; 723 AA.
ID      Q6EVR2
AC      Q6EVR2;
DT      01-MAR-2001 (TrEMBLrel. 16, Created)
DT      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      81-kDa leukemia toxin.
GN      Name=leuk81;
OS      Bacillus thuringiensis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_Taxid=1428;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=84-HS-1-11;
RX      MEDLINE=20342553; PubMed=10882663;
RA      Mizuki E., Park Y.S., Saitoh H., Yamashita S., Akao T., Higuchi K.,
RA      Ohba M.;
RT      "Parasporin, a human leukemic cell-recognizing parasporal protein of
RT      Bacillus thuringiensis."
RL      Clin. Diagn. Lab. Immunol. 7:625-634 (2000).
DR      EMBL; AB031065; BAB11757.1; -.
DR      InterPro; IPR005639; endotoxin N.
DR      InterPro; IPR008979; Gal bind like.
DR      Pfam; PF03945; Endotoxin N.1.
SQ      SEQUENCE 723 AA; 81045 MW; 2187358286B52 CRC64;

Query Match
Best Local Similarity 96.6%; Score 2473; DB 2; Length 723;
Matches 477; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy      1 IAEPSSTGYTTPRIINDNFIRIKYIAQLQSTNOSDIQYVLTPLPRAQCVWHMLLKDA 60
Db      232 MAEPSTGYITQFRILINDNFIRIKYIAQLQSTNOSDIQYVLTPLPRAQCVWHMLLKDA 291
Qy      61 TTSVWGQOIDSQOLNGYKAEILRLIKVYTNVDVNTYNOGLELEKAKPLVNSDPEETLQNG 120
Db      292 TTSVWGQOIDSQOLNGYKAEILRLIKVYTNVDVNTYNOGLELEKAKPLVNSDPEETLQNG 351
Qy      121 RPDISVLRSNFKVEMKMKVAKYKRGMAASLSIALPFTFGPNYKQALKVQSRLPA 180
Db      352 RPDISVLRSNFKVEMKMKVAKYKRGMAASLSIALPFTFGPNYKQALKVQSRLPA 411
Qy      181 PVIIGIPGGITTSODSGPTFGSMRPDVTKYTDIDALROLMLYIOLPKSAFYWIESDWKR 240
Db      412 PVIIGIPGGITTSODSGPTFGSMRPDVTKYTDIDALRLIMELYIOLPKSAFYWIESDWKR 471
Qy      241 ATTYVNDYIGKRSNTGAAMHMSDPSAITYTSALGAAGYAPNVVGRVSHGSGYTKGMAP 300
Db      472 ATTYVNDYIGKRSNTGLAMGMSDPSVITYTSALGAAGYAPNVVGRVSHGSGYTKGMAP 531
Qy      301 ANTNAVAPPEFYKPGYKLSVSAVGLSKAPDAADSVMGFRPVLLENANQLTDTALQI 360
Db      532 PNTNAVAPPEFYKPGYKLSVSAVGLSKAPDAADSVMGFRPVLLENANQLTDTALQI 591
Qy      361 PAEIGITDVPAFGRTBEEDINGODAIRIWEFTSGFTYVDSPOKQKXIIYRIANL 420
Db      592 PAEIGITDVPAFGRTBEEDINGODAIRIWEFTSGFTYVDSPOKQKXIIYRIANL 651
Qy      421 SASIVSLTYNNQTFPTDILNTSLDPNGVGNVGYTYLVEGPPIEFSGQINIFKLSQKGE 480
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Db      652 SASIVSLTYNNQTFPTDILNTSLDPNGVGNVGYTYLVEGPPIEFSGQINIFKLSQKGE 711
Qy      481 FAIDSIIFSPV 491
Db      712 FAIDSIIFSPV 722

RESULT 3
Q6BE06  PRELIMINARY; PRT; 829 AA.
ID      Q6BE06
AC      Q6BE06;
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      Cancer cell-killing Cry protein.
GN      Name=cry41ab1;
OS      Bacillus thuringiensis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_Taxid=1428;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=A1462;
RA      Yamashita S., Saitoh H., Katayama H., Akao T., Mizuki E., Park Y.,
RA      Ohba M., Ito A.;
RT      "Cell-killing toxin gene and other genes in 6,698bp DNA from Bacillus
RT      thuringiensis."
RL      Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB116651; BAD35163.1; -.
DR      GO; GO:0005102; F:receptor binding; IEA.
DR      GO; GO:0006952; P:defense response; IEA.
DR      GO; GO:0009405; P:pathogenesis; IEA.
DR      InterPro; IPR001178; Endotoxin.
DR      InterPro; IPR005638; endotoxin C.
DR      InterPro; IPR005639; endotoxin N.
DR      InterPro; IPR008979; Gal bind like.
DR      InterPro; IPR008997; Ricin B lectin.
DR      InterPro; IPR00772; Ricin B lectin.
DR      Pfam; PF03944; Endotoxin C_1.
DR      Pfam; PF00555; Endotoxin M_1.
DR      Pfam; PF03945; Endotoxin N_1.
DR      Pfam; PF00652; Ricin B lectin_3.
DR      SMART; SM00458; RICIN_1.
DR      PROSITE; PS50231; RICIN_B_LECTIN_1.
SQ      SEQUENCE 829 AA; 93861 MW; EBF1F3BEC05F97A3 CRC64;

Query Match
Best Local Similarity 9.5%; Score 244; DB 2; Length 829;
Matches 128; Conservative 86; Mismatches 210; Indels 152; Gaps 26;

Qy      9 VITQFRILN---DNFIKYIAQLQSTNOSDIQYVLTPLPRAQCVWHMLLKDA--S 63
Db      164 VLTERRNVNGHRENSMPSFAVRNFEVN-----LIPVVAEAMNHLILRLDAVKRGE 214
Qy      64 VMGQOIDSQOLNGYKAEILRLIKVYTNVDVNTYNOGLELEKAKPLVNSDPE-----EY 116
Db      215 GMSGSTDGAEKDDMYR-RLRSRTETIYDHCVNTYNOGLEQAKSLQANVSISRYEWTQY 273
Qy      117 LQAGRPDISVLRSNFKVEMKMKVAKYKRGMAASLSIALPFTFGPNYKQALKVQSRLPA 176
Db      274 NQSGGFSYREAKGEYRKMNNLVNAPFRDWTLLVLIDIAQPTYPDPGLYRPAVSELTFR 333
Qy      177 QIPAVVIGIPGGITTSODSGPTFGSMRPDVTKYTDID--ALRQI-----MELYIQP 224
Db      334 EYVYTDIRG-----TTWSDANLITIDAIENRMVGSROLQFTWLTMEKFIYRN 381
Qy      225 LKSAFWIYIES-----DMKVATYVND-YIGKRSNTGA-----MH----- 260
Db      382 TGSITSYTHGDLNGLGEEKIKRTNDNDQWPLEGQNTSYTRIIRDPGIELGNVWYARQ 441
Qy      261 -----MW-SSDPSAITYTSALGAAGYAPNVVGRVSHGSGYTKGMAPANTNAVAPPE 310
Db      442 QMFETRLQLQWNTDVLSLNGCTYGNEMFADVDVPRNRIYARSTNNHIEHRLSWIKFE 501
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CC -----  
DR EMBL; M64478; AAA22351.1; -;  
DR EMBL; A07236; CAA00646.1; -;  
DR PIR; A48944; A48944.  
DR HSSP; P07130; 1DLC.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; Endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR Pfam; PF03944; Endotoxin\_C; 1.  
DR Pfam; PF00555; Endotoxin\_M; 1.  
DR Pfam; PF03945; Endotoxin\_N; 1.  
DR Spoolation; Toxin.  
QO SEQUENCE 1138 AA; 129391 MW; 69D8676D4FEA1FAC CRC64;

Query Match	8.9%;	Score 228.5;	DB 1;	Length 1138;
Best Local Similarity	22.4%;	Pred. No. 5.7e-08;		
Matches 124;	Conservative 70;	Mismatches 216;	Indels 143;	Gaps 23;

Qy	9	VITOPFRINDNEIKYIAKIQFSTNOSDDO-YPLLTPLPAQCMHMLMLKATTT--SW	65
Db	157	VATERRIIDSLF-----EFMSPRKTYGIELPLLTVAQAQANHLALLRSDTLTGDKM	209
Qy	66	G--QQIDSOQLNGVYAEELIRLIKVTYNDVNVTYNOGLELEKAKPLNYSDEEYLQGRPD	123
Db	210	GFTQNNIEENYNRQK---KRISEYSDHCTKWNSGLS-----	243
Qy	124	ISVLRSNKEVWKMKVAKYKRGMSALSLAEPFPPGNPKALXVVSQRIAPVY	183
Db	244	---RLNSTYEOWINYNRFRREMTIMLADLVAVFPFHDPRRYSMETSTQLTREYVTDPV	299
Qy	184	GIPGGITQODSGPTEGSM-RFDVUKTYDQIDALROLMELYIQPLKSAFWIYESDMKVRAT	242
Db	300	SL--SISNPDIGSPFSQMENTAIRPHVLVDIDEL-----YIYISKYAFSH	344
Qy	243	YVNDYIGKRGSGNTGAAMHMS-----SDPSAITSAL--GAAGYAPNVGVRSYHGG	292
Db	345	EIQPDL-----FYMSAHKVSFKKSEOSNLTYYTIGYKTSGYISS--GAVSFHGN	391
Qy	293	SYTKMAPANTVAVAPFEKYP---GYKLHSAVAYL-----SKAPDADSVW	337
Db	392	DIYRILA-----APSVVVVYPTONYGYEYQVEYFGVKGHHVYRGDNKYDLYDSIDQIP	444
Qy	338	FGFRFVLLLENANQLITDPAIQPAEIGITTDVVPARGTE-----BEINGQDAI	386
Db	445	PDGEET-HEKYTHRLCHATAIRFKSPDPYDNATPIEFMSVHRSAEVYNNRIYPNKITMIPAV	503
Qy	387	RIWE-----SFTSGGFGFT-----YTDSPOKQOKYKIIYRIANLNSAST	424
Db	504	KMYKLDDESTVAVKGGFTGDLVKRGSTGYIGDIKATVNSPLSQKYRVHVRAYATVNSGOF	563
Qy	425	VSLTNNQCTFFPDILNT-SLDPNGVRGNNGSYTIIV-GRILIESQGTNIFPKG----	504
Db	564	NYIINDKLTILQTKPONTVEETIEGKDLTYGSGYIEYSTTIOEPDEHPKITLHLSDLNN	623
Qy	479	GEFAIDSIIFSPV	491
Db	624	SSFYVDSTIEFLIV	636
RESULT 6			
C7AB_BACUA			
ID	C7AB_BACUA	STANDARD;	PRT; 1138 AA.
AC	045707;		
DT	16-OCT-2001	(Rel. 40, Created)	
DT	16-OCT-2001	(Rel. 40, Last sequence update)	
DT	05-JUN-2004	(Rel. 44, Last annotation update)	

```

DE Pepticidial crystal protein cry7Ab (Insecticidal delta-endotoxin
DE CryVIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN Name=cry7Ab; Synonyms=cryVIA(b);
OS Bacillus thuringiensis (subsp. akroca).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132268;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD511;
RA Payne J.M., Fu J.M.;
RT "Coleopteran-active Bacillus thuringiensis isolates and genes encoding
RT coleopteran-active toxins.";
RL Patent number US5286486, 15-FEB-1994.
CC -I- FUNCTION: Promotes colloid-osmotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC
CC -I- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC -  
DR EMBL; U04367; AAA21120.1; -.  
DR HSSP; P07130; 1DLC.  
DR InterPro; IPR001178; Endotoxin.  
DR InterPro; IPR005638; endotoxin\_C.  
DR InterPro; IPR005639; endotoxin\_N.  
DR InterPro; IPR008979; Gal\_bind\_like.  
DR Pfam; PF03944; Endotoxin\_C\_1.  
DR Pfam; PF00555; Endotoxin\_M\_1.  
DR Pfam; PF03945; Endotoxin\_N\_1.  
DR Spoolation; Toxin.  
KW SEQUENCE 1138 AA; 129778 MW; 01DF072C074CE88 CRC64;  
SQ

Query Match	8.8%;	Score 225.5;	DB 1;	Length 1138;
Best Local Similarity	22.5%;	Pred. No. 9.5e-08;		
Matches 126;	Conservative 75;	Mismatches 207;	Indels 151;	Gaps 25;

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0Y      TGVITQERLINDEFKYLAKOFNSQSDLOYPIVLTPLEPAQACWHEMLMLKQAT--SV 64
Db      155 TRIDRFRLLDALFESYMSFRVA-----GYEIPLTVYAQAANLHALIRBOSTLYGDK 208
0Y      65 WG--QOIDSQOLNGYKABELIRLIKVTYNDVNTYNOGLELEKAKPLNYSDEEYLQAGR 122
Db      209 WGFQNNIEENYNRQK---KHISEYSHKCVKWNNGSL-----243
0Y      123 DISVLASNKEKEMKNNKAKYKRGMAABSLALPFEFGNYPKALKTQVSSROIFAPV 182
Db      244 ----FLNASTYEQWNTNFRFRREMLIWLIDIAVFLPYDRMYSMETSTQLTREYVTD 238
0Y      183 IGIPEGITQSODSGPFGESWRFDV--LTYQOIDALROLMELYIOLPK-----SAYFW 231
Db      299 ISL--SISNPDIGSPSQCMENTAPFTPLHVD--YLBELVIYLSKYKAFSHEIQPDLFEW 353
0Y      232 -IYESPMKYRATVYNDYIGKRGSGNTGAAMHMSDPSALYTSAL--GAAGYAPNVGVRY 288
Db      354 CVKHVSFFK-----KSEOSNLVTTGYTGKTSY-----ISSGAY 386
0Y      289 SHGGS--YTKGMAPA-----NTNAYAPEPFYPCGKJH---SVSAYGLSKAPDAASVM 337
Db      387 SFGANDIYKTLAPSVVYPTQYNGVQVEFYGVKGVHVRGDKNDLTY--DSIDQLP 444
0Y      338 FGRFVLLNEANQLLTDALQIPAEIGITDVVPAFGTE-----EPINGDAL 386

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GN Name=CRY42Aa1;
OS Bacillus thuringiensis.
OC Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AL62;
RA Yamashita S., Satoh H., Katayama H., Akao T., Mizuki E., Park Y.,
RT "cell-killing toxin gene and other genes in 4.567bp DNA from Bacillus
RT thuringiensis."
RL Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB116652; BAD3166.1; -
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005639; endotoxin_C.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR008997; RicinB like.
DR InterPro; IPR007772; Ricin_B_lectin.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF00555; Endotoxin_M_1.
DR Pfam; PF03945; Endotoxin_N_1.
DR Pfam; PF00652; Ricin_B_lectin; 3.
DR SMART; SM00458; RICIN_1.
DR PROSITE; PS50231; RICIN_B_LECTIN; 1.
SQ SEQUENCE 810 AA; 91300 MW; 61D27179220D249B CRC64;

Query Match 8.3%; Score 211.5; DB 2; Length 810;
Best Local Similarity 23.3%; Pred. No. 6,6e-07;
Matches 133; Conservative 81; Mismatches 210; Indels 147; Gaps 29;

QY 2 AEPSTGVITQRIINDNFIXIAKLQSTNQSDIQYPLTLPLRAQACWMLMLKDAT 61
DB 158 SEPIQRLQSLQPTANTFTIVGSMISFRVGRH---EVLPLT--TFVQANLHLILLRDAI 211
QY 62 T--SVWGQIDISQALNGYKAEILIRIKYTTNDVNTTNOGLEAKPLNYSDPREYQA 119
DB 212 MFGESWG--MCPVTVAGYQDNFNMRNRIADYTVSVIVNQGLQAKTTLTANLRDEKYQWA 269
QY 120 GRPDSV--LRSNFKVKMKNKVAKYKRGMAASLSLALFPFGNRYKQALKVQSRQI 178
DB 270 RYVNSVPEBPAFYAGMENWNLNYYNRDMTLVTLVALMPTYNQOYPIAKIQLITKEI 329
QY 179 FAPVIGIPGIGITSDSGPTFGSMRPDVKYQIDALROLMEIYIQLPLSAFYWIESD-- 236
DB 330 YTELKGNMGN--TKRS-----MDALDA-----ELI--PPRLFTWLESVDMH 368
QY 237 -WKVRA-----TYVNDYIGKRGSTNGAAMHMSDPSALYTSALGAAGYAPNVV----- 284
DB 369 RWPISAGYVYTFQNAIGIKHR-----YKYLDSQTLTSLRGASGNFNLVPAERTI 420
QY 285 -GVRSHG--GSYT-----KGNAP-----ANTNAVAP-----EKKPYGYLH--- 319
DB 421 NKVQOHGBGLTFPSFRSGSDPLNIGTIDKDKYVSTNARI PVEGDOQTQANHRLSWIT 480
QY 320 -----SVSAYGLSKAPDAADSVMFGEFVLLNEANQLTDTALQIPAEIGI-----T 367
DB 461 GMVITELSLIPAFG--HYNPITYISCAEGWTHLSVE--RSNEIKSDKITQIPAVYAFQLSNNA 538
QY 368 DVPAFGRTPEPINOADAIRIWESFTSGFGFTY-----TDSFKQKKYKIIYRIANLU-- 420
DB 539 SVVRGPGST-----GGDLVQ--FSATSSGNKQLMIKVKPTTIALGRFPKRIIRYAAAANVT 592
QY 421 -----SASTVSLTVN-----NOTFFDILNTSLDNGVRYGNVGSYTLVWG 460
DB 593 FTVQACVTVGACWETATKSVITTYISGTLTVNAFKYVDLFE-----IPANSEPSL--- 642
QY 461 PLIEFSOGTINIFKLGSOKGEFAIDSIIPSPV 491
DB 643 ---EF-----LSTSGGPYIYIDKIEFIIV 662

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RESULT 11
C1A_BACTU
ID C1A_BACTU STANDARD; PRT; 1167 AA.
AC Q45738;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIIA (Insecticidal delta-endotoxin
DE CryII(a) (Crystalline entomocidal protoxin) (133 kDa crystal protein).
GN Name=CryIIA; Synonyms=CryET4, CryII(a);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryeta and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects."
RL Patent number US5322687, 21-JUN-1994.
CC -1- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -1- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L32019; AAA2241.1; -
DR HSSP; P02965; IC1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF00555; Endotoxin_M_1.
DR Pfam; PF03945; Endotoxin_N_1.
KW Sporulation; Toxin.
SQ SEQUENCE 1167 AA; 132760 MW; 3B7357D14E655FC7 CRC64;

Query Match 8.2%; Score 210.5; DB 1; Length 1167;
Best Local Similarity 21.9%; Pred. No. 1.3e-06;
Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

QY 3 EPPSTGVITQRIINDNFIXIAKLQSTNQSDIQYPLTLPLRAQACWMLMLKDAT 62
DB 123 EAKSRVLDRIIRLLDGLIENATPSFRI-----IGFVPLLSVYVQANLHLIRDSV- 175
QY 63 SVWGQ--IDSQALNGYKAEILIRIKYTTNDVNTTNOGLEAKPLNYSDPREYQAG 120
DB 176 -IFGRMGLTTKNVNDIYNRQIREIHEYSNHCVDTYNTELE----- 215
QY 121 RPDISVLSNFKVKMKNKVAKYKRGMAASLSLALFPPTGEN--YPKQALKVQSRQIF 179
DB 216 -----RLGFRSLAQWRIYVQFRRELTLVTLVIALFPNYSRLYPIQTFPSQLTRELIVT 268
QY 180 APVIGIPGIGITSDSGPTFGSMRPDVKYQIDALRLQ-----MELYIQLKSAFYW--- 231
DB 269 SPVSEFYYGVI--NSGNITGL-----TEQDIRPPLMDPNSMIMTISDNKREHYMSGL 321
QY 232 --LY-----ESDWKVRATTVND-----YIGKR 251

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DB 322 EMTAVFTGFAQVQSPFLVGTGEGSAPPLITVASVNDGIYRILISAPFYSAFLGTVLQSR 381
QY 252 GSNTGAAMHMMSSDPSAIYTSALGAGYAPNVGVRYSHGSGYTKGMAPANTNAYAPPEF 311
DB 382 GEKFDLANNISPPSTIYR---PGTVDSLVI-----PQONSVP--- 421
QY 312 KYPGYKLHVSAYGSKAPDAADSVMEGF--RPVLEENANQLDITLQIAEIGTIDV 369
DB 422 -----HRGSSHRISHVTMRASSPFFHWTHRSATTTNTIN--PNAIIQIP-----L 464
QY 370 VPAFGRTEEPINGODAIRIMESFTSGFGFT-----YTVDSPQOKYKI 412
DB 465 VQAFPLH-----SGATVVR-----GPGTTGDIARRTNTGPFADMKNVITGSLQRIYV 513
QY 413 IYRIANNLSASTVSLTYNNQTFETDILNTSLDPNGVGNVGSYTLVEGPILF----- 464
DB 514 RIRY-----ASTTDL-----QFFTRINGTSVN-----QGNF--QRTMNRGDNLESNGNFRTAG 558
QY 465 -----FSGGTNIFFKLGSG--KGEFADISLIIFSP 490
DB 559 FSTPFSFSAQSTFTLTGTQAFSNGQEVYIDRIEFVP 593

RESULT 12
CIFB_BACTM STANDARD; PRT; 1169 AA.
ID CIFB_BACTM
AC 066377; Q9RC19;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIpb (Insecticidal delta-endotoxin
GN cryIpb) (Crystalline entomocidal protoxin) (132 kDa crystal protein).
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang Z., Ding Z., Chen Z., Li G., Huang D.;
RT "A novel cryIpb gene from Bacillus thuringiensis subsp. morrisoni.";
RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=INA67;
RC Maesuda K., Asano S.;
RL Submitted (Mar-1998) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: Promotes colloidal osmotic lysis by binding to the midgut
epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF062350; AAF21767.1; -
CC EMBL; AB012288; BAA25298.1; -
CC HSSP; P02965; 1C1Y.
CC InterPro; IPR001178; Endotoxin.
CC InterPro; IPR005638; endotoxin_C.
CC InterPro; IPR005639; endotoxin_N.
CC InterPro; IPR008979; Gal bind like.
CC Pfam; PF03944; Endotoxin_C_1.
CC Pfam; PF00555; Endotoxin_M_1.
CC Pfam; PF03945; Endotoxin_N_1.
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KM Sporulation; Toxin.
FT CONFLICT 338 338 V -> I (in Ref. 2).
FT CONFLICT 382 382 G -> A (in Ref. 2).
FT CONFLICT 1002 1002 V -> I (in Ref. 2).
FT CONFLICT 1012 1012 E -> K (in Ref. 2).
FT CONFLICT 1053 1053 Missing (in Ref. 2).
FT CONFLICT 1085 1085 G -> R (in Ref. 2).
SQ SEQUENCE 1169 AA; 132284 KM; EPCAF6F6E7BC1E CRC64;

Query Match 8.1%; Score 207.5; DB 1; Length 1169;
Best Local Similarity 22.7%; Pred. No. 2,1e-06;
Matches 131; Conservative 77; Mismatches 200; Indels 169; Gaps 30;

QY 10 ITQRIILDNFIKIYAKL-QFTNQSDIQ-----YFVL 41
DB 95 ITTLRGLDSEYEVLEALREWEENPNNAQLREDRVIRFPAITDALLITAINFFTLTSFEIP 154
QY 42 TLPLRAQACVWMLMKQATTSVWGQQLDSQQLNGYKALIRLKYVINDVNTYNNQGLE 101
DB 155 LLSTVYQANLHLSLRLDAVSFGQGWGIDLATVNNHYNRLINLIRYEHCLDITYNQGLE 214
QY 102 LEKAPLNVSDPEEYLQGRPDISVLRSNPFKEWKMNVAKYKRGMAASLSLALPPTF 161
DB 215 -----NLRGNTNQ---MSRFNQPRRELTLTVLDIYALFPNY 248
QY 162 GPN-VPKQALKVQSRQIF-----APV-IGIPGITSQDSGPTFGSMRPDVKTYYQID 212
DB 249 DARAVPIQTSSQL-TREIYTSVIEDSPVSANIPNG-----FNRAEFGVAPPHLMD 298
QY 213 ALRQLMELIYIPLKASATW--IYSDMKVRYATVNDYIGKRGSTNGAAMHMMSSDPSAIY 270
DB 299 FWNLSLF-VTAATVVSQTVWGCHLVSSRNTAGNPINFPYGVNPGGALW-TADEDPPEFY 356
QY 271 TS-----ALGAAGYAPNVGVV--YSHGSGYTKGM-----APANTNAYAPF 309
DB 357 RFLSDPVVRVGFGFQGNPHVVLGLRGVPGQGTNTNTRTFRNSGTDLSDEIIPQNSGAPW 416
QY 310 E-----FRYPGYKLHVSAYGSKAPDAADSVMEGPRVYLENEANQLITLTAAL 358
DB 417 NDYSHVLNHTVFWVPG---EIASDSWRAP-----MFSWTH-RSADRTNIINPNIIT 465
QY 359 QIPA-----BIGITDV-VPAFGRTEEPINGODAIRIMESFTSGRG-FTYVDSPOKQY 410
DB 466 QIPAVKANLHSGSTVVRGPGF-----TGDGLR-RITVGTFFADIRAVNITGSLQRY 516
QY 411 KIYRIANNLSASTVSLTYNNQTFETDILNTSLDPNGVGNVGSYTLVEGPILF----- 464
DB 517 RVRIRY-----ASTTDL-----QFFTRINGTSVN-----QGNF--QRTMNRGDNLESNGNFR 561
QY 465 -----FSGGTNIFFKLGSG--KGEFADISLIIFSP 490
DB 562 AGFSTPFSFSAQSTFTLTGTQAFSNGQEVYIDRIEFVP 598

RESULT 13
Q45749 PRELIMINARY; PRT; 1174 AA.
ID Q45749;
AC Q45749;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 03-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Crystal protein (Crystal delta-endotoxin).
GN Name=cryIpb;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Lambert B.;
RL Submitted (Apr-1993) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B-Pf-86;
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OX NCBI_TaxID=1433;
RN [1]
RC STRAIN=EG6346;
RX MEDLINE=91286178; PubMed=2061280;
RA Chambers J.A., Jelen A., Gilbert M.P., Jany C.S., Johnson T.B.,
  Gawron-Burke C.,
RT "Isolation and characterization of a novel insecticidal crystal
  protein gene from Bacillus thuringiensis subsp. alzawai.";
RL J. Bacteriol. 173:3966-3976(1991).
RN [2]
RC STRAIN=NRL-B-18484 / P6811;
RA Payne J.M., Sick A.U.;
RT "Bacillus thuringiensis isolate active against lepidopteran pests, and
  genes encoding novel lepidopteran-active toxins.";
RL Patent number US5188960, 23-FEB-1993.
CC -! FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
  epithelial cells of many lepidopteran larvae.
CC -! DEVELOPMENTAL STAGE: The crystal protein is produced during
  sporulation and is accumulated both as an inclusion and as part of
  the spore coat.
CC -! MISCELLANEOUS: Toxic segment of the protein is located in the N-
  terminus.
CC -! SIMILARITY: Belongs to the delta endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M63897; AAA22348.1; -
DR EMBL; M73254; AAA22347.1; -
DR PIR; A42459; A42459.
DR HSSP; P02965; 1C1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF00555; Endotoxin_M_1.
DR Pfam; PF03945; Endotoxin_N_1.
DR Sporulation; Toxin.
SQ SEQUENCE 1174 AA; 133621 MW; B51B9751D7F91C61 CRC64;

Query Match 7.8%; Score 200; DB 1; Length 1174;
Best Local Similarity 22.0%; Pred. No. 7.8e-06;
Matches 127; Conservative 79; Mismatches 204; Indels 168; Gaps 29;

OY 10 ITQPRILNDNFIKYIAKL-QFSTNOSDLQ-----YPLV 41
DB 95 ITTLGLADSYEIIYEALEMEANPNNAQLREDEVRIKRPANTDALTAINNFTLSFEIP 154
OY 42 TLPLBAQACVMHMLIKDATTSVWGOQIDSOQINGYKAEILRLIKYITNDVNTYNOGLE 101
DB 155 ILSVYVQAANLHLISLRDAVSFGQGWGLDIATVNNHYNRLINLHRYTGHGCLDTYNOGLE 214
OY 102 LEKAPKINSDPEBEYQAGRPDISVLRSPKVEVMKKNKAKYKRGMAAGLSIALFPTF 161
DB 215 -----NLKGTNRQ---WARFNPQRRDLTLTLVDIVALFPNY 248
OY 162 G-PNYPKQALKVQSHQIF-----APY-IGIPGGITSQDSGPTFGSMKFPDVKYDQID 212
DB 249 DVRTYPIQITSSQL-TREITSSVIEDSPYSANIPNG-----FNRAFGVRRPHLMD 298
OY 213 ALRQIMELYIQPKSAYFWIYSDMKVRATYVNDYIGKRG-----NTGAAMHMSSD 265
DB 299 FNNSLF-VTAETVRS-----QTVMGHILVSSRNTAGNRINFPSSYGVFNPGAIWIADBD 351
OY 266 PSAITS-----ALGAGIAPNVGVV-----YSHGGSYTKGM-----APANTN 304

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DB 352 PRPFYRTLSDPVVRKGGFGNPHYVLGLRGVAFQOTGNTHTFNRNSGTIDSLDEIIPQDN 411
OY 305 AYAPPE-----FKYPGYKLHSVASAYGLSKAPPAADSVMEGFPVLLNEANQL 353
DB 412 SGAPWNDYSHLVNHTFVRWPG-----EISGSDSWRAP-----MPSWTH-RSATPTNTID 460
OY 354 TDTALQIP-----AEIGITDV-VPAFGRTPEEPINGODAIRIWESFTSGFGFTYTV---- 402
DB 461 PERITQIDPLVRAHTLOSSTTVVRGPGF-----TGCDILR-----RTSGGPFAYTIVNIN 509
OY 403 -DSPQKQKKXIIRANLNSASTVSLTYNNQTFPTDINTSLDPNGVAGNGSY----- 455
DB 510 GQLPQRYRARIKYASTNL---RIVTVAGRIEIPAGQFNKTMW-TGDPPLTFQSFYSYATIN 565
OY 456 TLVEGPITE--FSQGTNIFKLGSQKGEPAIDSIIFSPV 491
DB 566 TATFPMSGSFTVADTFSSGN---EYIDRFELIP 600

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Search completed: October 19, 2005, 20:17:43  
Job time : 182 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 19, 2005, 20:08:58 ; Search time 44 Seconds  
(without alignments)  
834.712 Million cell updates/sec

Title: US-10-756-778-8  
Perfect score: 2560  
Sequence: 1 IAEPPSTGVITQFRLINDNF.....KLGSQKGFALDSITFSPV 492

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pdp:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pdp:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pdp:\*  
5: /cgn2\_6/ptodata/1/1aa/6C.COMB.pdp:\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	225.5	8.8	1138 1	US-07-973-320-2
2	225.5	8.8	1138 1	US-07-973-320-4
3	223.5	8.7	1169 1	US-08-542-921-2
4	223.5	8.7	1169 2	US-08-880-685-2
5	223.5	8.7	1169 2	US-08-880-684-2
6	210.5	8.2	1167 1	US-08-100-709-2
7	210.5	8.2	1167 1	US-08-176-865-2
8	210.5	8.2	1167 1	US-08-474-038-2
9	210.5	8.2	1167 2	US-08-779-046-2
10	210.5	8.2	1167 2	US-08-881-340-2
11	207.5	8.1	1168 1	US-08-291-368-4
12	207.5	8.1	1168 2	US-08-962-190-4
13	207.5	8.1	1168 5	PCT-US95-10310-4
14	200	7.8	605 3	US-09-178-252-4
15	200	7.8	605 4	US-09-826-660-4
16	200	7.8	718 2	US-08-731-079A-1
17	200	7.8	1148 1	US-08-349-867-23
18	200	7.8	1148 1	US-08-349-867-23
19	200	7.8	1148 1	US-08-239-476-23
20	200	7.8	1148 1	US-08-239-476-23
21	200	7.8	1148 2	US-08-598-305A-23
22	200	7.8	1148 2	US-08-598-305A-27
23	200	7.8	1148 2	US-08-598-305A-35
24	200	7.8	1148 2	US-08-598-305A-37
25	200	7.8	1148 2	US-08-598-305A-38
26	200	7.8	1148 2	US-08-639-923A-23
27	200	7.8	1148 2	US-08-639-923A-27

28	200	7.8	1148 2	US-08-639-923A-35	Sequence 35, Appl
29	200	7.8	1148 2	US-08-639-923A-37	Sequence 37, Appl
30	200	7.8	1148 2	US-08-639-923A-38	Sequence 38, Appl
31	200	7.8	1148 3	US-09-178-252-2	Sequence 2, Appl
32	200	7.8	1148 4	US-09-826-660-2	Sequence 2, Appl
33	200	7.8	1148 5	PCT-US95-05431-23	Sequence 27, Appl
34	200	7.8	1148 5	PCT-US95-05431-27	Sequence 10, Appl
35	200	7.8	1174 1	US-07-828-788A-10	Sequence 25, Appl
36	200	7.8	1174 1	US-08-349-867-25	Sequence 29, Appl
37	200	7.8	1174 1	US-08-349-867-29	Sequence 32, Appl
38	200	7.8	1174 1	US-08-349-867-32	Sequence 29, Appl
39	200	7.8	1174 1	US-08-239-476-25	Sequence 29, Appl
40	200	7.8	1174 1	US-08-239-476-29	Sequence 25, Appl
41	200	7.8	1174 2	US-08-356-034-8	Sequence 29, Appl
42	200	7.8	1174 2	US-08-598-305A-25	Sequence 32, Appl
43	200	7.8	1174 2	US-08-598-305A-29	Sequence 32, Appl
44	200	7.8	1174 2	US-08-598-305A-32	Sequence 25, Appl
45	200	7.8	1174 2	US-08-639-923A-35	Sequence 25, Appl

# ALIGNMENTS

RESULT 1  
US-07-973-320-2  
Sequence 2, Application US/07973320  
Patent No. 5286486  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel M.  
TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene  
TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/973,320  
FILING DATE: 19921106  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/788,638  
FILING DATE: 6-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
TELEPHONE: 904-372-5800  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1138 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus thuringiensis  
STRAIN: dakota  
INDIVIDUAL ISOLATE: HD511  
IMMEDIATE SOURCE:

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1      LIBRARY: Lamsdgem (TM) -11 Library of J.M. Fu
2      CLONE: 511
3      US-07-973-320-2
4
5      Query Match      8.8%; Score 225.5; DB 1; Length 1138;
6      Best Local Similarity 22.5%; Pred. No.1.1e-12;
7      Matches 126; Conservative 75; Mismatches 207; Indels 151; Gaps 25
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9      QY      7      TGVITPPIIANDNFIKIYAKLOFSTNSDLOQPVLTLEPRAQCVNHLMLKDATP--SV 64
10     Db      155     TRVIDRFRIIDLAFESYMPSEFVA-----GYEIPLTIVYAQAANHLALLRDSSTLYGBK 208
11
12     QY      65      WG--QIDISQOLNGKAEILIRIKYTYNDVNTTNOGLEBEAKKPLNTSDPEEYIOAGRP 122
13     Db      209     WGFTONNIEENNRK---KHISEYSHCVKYNVSGS-----243
14
15     QY      123     DISVLSNFKFEVMKNNKAYKRGKAMASLSIALFPFGPNVYKQALKVYOSRQIFAV 182
16     Db      244     -----RNGSTYEQINNNRFRREKILMWLDIAAVFPYIDPRMYSMEISTOLTREYTPD 298
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18     QY      183     IGIPGIGITSODSGPTFGSMRFDV-KTYDQIDALRLMELIYIOPK-----SAYFW 231
19     Db      299     ISL--SISNPDIGPFSQOMENAFRTPLHVD--YLDLXYITSKYKAFSHEIQPDLFYW 353
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21     QY      232     -IYESDMKVRATYVNDYIGKGSNTGAMHMMSSDPSALYTSAL--GAAGYAPNVGVRY 288
22     Db      354     CVHKASFK-----KSEOSMLYTTGIIGKTSGY--ISSGAY 386
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24     QY      289     SHGGS--YTKGMAPA-----NTNAYAPFEKYPGYKLIH--SVSAVGSKAPDAADSVM 337
25     Db      387     SFRGNDIYRTLAABSVVYPTQNTGVGEVEYGVKGVHNYRGDKYDLTY--DSIDQLP 444
26
27     QY      338     FGFRPVLLENEANQLLTDTALQIPAEIGITDVVPFGRTE-----EPINGODAI 386
28     Db      445     PDGEPI-HEKXTHRLCHATAIKSPDYDQNAITPIFSWTHRSABEYNNRIYPMKIKKIPAV 503
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30     QY      387     RIWE-----SFTSGGFT-----YTDSPOKOKYKTIYRIANNLSA-- 422
31     Db      504     KMYKLDLSTVVKGPGFTGGDLVKRGSNGYIGDIKATVNSPLSQKRVAVRYATSVSGLF 563
32
33     QY      423     ---STVSLVYNNQTFPFDILNTSLDPNGVAGNGYSYTLVE-GPIIESQGTNIFKG- 475
34     Db      564     NVFINDEIALQKNFQSTVETI-----GECKDLTYSFYEIYESTTIOPEHNEPKITLHL 617
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36     QY      476     --SOKGEFAIDSIIFSPV 491
37     Db      618     NMLSNNSPFYVDSIEFIV 636
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39     RESULT 2
40     US-07-973-320-4
41     Sequence 4, Application US/07973320
42     Patent No. 5286486
43     GENERAL INFORMATION:
44     APPLICANT: Payne, Jewel M.
45     APPLICANT: Fu, Jenny M.
46     TITLE OF INVENTION: No. 5286486e1 Bacillus thuringiensis Gene
47     TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
48     NUMBER OF SEQUENCES: 4
49     CORRESPONDENCE ADDRESS:
50     ADDRESSEE: David R. Saliwanhik
51     STREET: 2421 N.W. 41st Street, Suite A-1
52     CITY: Gainesville
53     STATE: FL
54     COUNTRY: USA
55     ZIP: 32606
56
57     COMPUTER READABLE FORM:
58     MEDIUM TYPE: Floppy disk
59     COMPUTER: IBM PC compatible
60     OPERATING SYSTEM: PC-DOS/MS-DOS
61     SOFTWARE: PatentIn Release #1.0, Version #1.25
62     CURRENT APPLICATION DATA:
63     APPLICATION NUMBER: US/07/973.320

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1      FILING DATE: 19921106
2      CLASSIFICATION: 435
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: US 07/788,638
5      FILING DATE: 6-NOV-1991
6      ATTORNEY/AGENT INFORMATION:
7      NAME: Salivanchik, David R.
8      REGISTRATION NUMBER: 31,794
9      REFERENCE/DOCKET NUMBER: M468.C1
10     TELECOMMUNICATION INFORMATION:
11     TELEPHONE: 904-375-8100
12     TELEFAX: 904-372-5800
13     INFORMATION FOR SEQ. ID NO. 4:
14     SEQUENCE CHARACTERISTICS:
15     LENGTH: 1138 amino acids
16     TYPE: AMINO ACID
17     STRANDEDNESS: single
18     TOPOLOGY: linear
19     MOLECULE TYPE: protein
20     HYPOTHEetical: YES
21     AMTI-SENSE: NO
22     ORIGINAL SOURCE:
23     ORGANISM: Bacillus thuringiensis
24     STRAIN: kumamocensis
25     INDIVIDUAL ISOLATE: HD867
26     IMMEDIATE SOURCE:
27     LIBRARY: Landagem (TM)-11 library of J.M. Fu
28     CLONE: 867
29     US-07-973-320-4

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Query Match	8.8%;	Score 225.5;	DB 1;	Length 1138;
Best Local Similarity	22.5%;	Pred. No. 1.1e-12;		
Matches 126;	Conservative 75;	Mismatches 207;	Indels 151;	Gaps 25

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QY      7 TGIITQFRLINONFLIKYIAKQFSTNOSDLOQPVULTLPLAQAQVCHMLMLKXQATT--SV 64
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QY      65 WG--QQIDSOQNGKAEILIRLIKYYTNDVNTYNOGLEEKAPLKYVSDPEEYLOAGR 122
Db      209 WGTQNNIEENNRQK-----KHISYSHCHVKWNSGLS-----243
QY      123 DISVLRSNFEKVMKNNKVAKYKKGAMASLSLALPFTGPNTPKQALKVQSRQIFAPY 182
Db      244 -----RLNSTYEQWQINNRFRREMLMVLIDIAAVFPIYDPRMYSMETSTQLTREYVTD 298
QY      183 IGIPIGITSQDSGPFPGSMRPDY-KTYQIDALQOMELTYQPK-----SAYFW 231
Db      299 ISI--SISNPDIGSPFSQMENTAFETPLVD--YLBELIYTSKYKAFSHEIOPDLFEW 353
QY      232 -IYESDMKRYRAYVNDYIGKRGSNTGAMHMSDDPSAIYTSAL--GAAGYAPNVGVRY 288
Db      354 CHAKUSFK-----KESQNSLITTTGTYGKTSSEY--ISSGAY 386
QY      289 SHGGS--YTKGNAPA--NTNAYAPPEFYKPGYKYLH--SVSAYGLSKAPDAADSVW 337
Db      387 SFGNDNIYRTLLAPSVVVYPTQYNGVQGEVFGVKGHVHYRGDKNYDLTY--DSIDIQL 444
QY      338 FGRRPILLENANOLLTLOTALQIPAEIGITDVVVAFGTE-----EPINGDAI 386
Db      445 PDEEPI-HEKYTHIRCHATAIASKSTPYDYNATIPIFSWTHRSAEYNNRIYPNKIKIIPAV 503
QY      387 RIWE-----SPTSGGFGFT-----YVDSPOKQKYIIRIANNLSA--422
Db      504 KMKIKDDLSTVVKGGGFTGGDLYKRGNSNGYIGDIKATVNSPELSOKRVRVRYVTSVGLF 563
QY      423 -----STVSLTYNNQTFPTDILNLTSLDPNGVRGVNGYSYTLVE-GRPIEFSQTNIFPLG- 475
Db      564 NVFINDIELMQLQNFQSTVETI-----GEGKDLVYGSFGVIEYSTTITQFNEHPKITTLLH 61.7
QY      476 ---SOKGEPAIDSIITSPVY 491
Db      618 NHLJNNSPFYVDSIEFIIV 636

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RESULT 3  
US-08-542-921-2  
; Sequence 2, Application US/08542921  
; Patent No. 5736514  
; GENERAL INFORMATION:  
; APPLICANT: IIZUKA, TOSHIHIKO  
; APPLICANT: TAGAMA, MICHITO  
; APPLICANT: ARAI, SATOSHI  
; APPLICANT: MIIZEKI, MASATSUGU  
; APPLICANT: MIYAKE, TOSHIRO  
; TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL  
; TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/542,921  
; FILING DATE: 13-OCT-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 276082/94  
; FILING DATE: 14-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 49-209-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1169 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-542-921-2

Query Match 8.7%; Score 223.5; DB 1; Length 1169;  
Best Local Similarity 22.3%; Pred. No. 1.8e-12;  
Matches 130; Conservative 78; Mismatches 192; Indels 183; Gaps 30;

QY 9 VITQRIINDNPRIKIALQFSTNSDQYPLVTLPLRAQACVMMILMKATT--SVWG 66  
DB 168 VSQRNILDLSLFTQFMP--SFSGSGSQNYATILPLVYAQANLHLLELKLDIYGAWG 225  
QY 67 QOIDEQQLNGYAKELIRLIKVTNDVNTYNOGLELEKAKPLANYSDPEEYLQAGRPIISV 126  
DB 226 --LWQTQIDQPHSRQOSLTQYITNHCVTAYNDL-----AE 259  
QY 127 LRSNFEVWKNNKVAKYKGMASALSLALPPTGPNYPKQALKVQSRQIFAVIGI- 185  
DB 260 LRGTTAE--SWFKYQYRREMTLTAMDIALPYPYNLQYPPDGTNPOLTRREYVTDPIAFD 317  
QY 166 -----PGGITSQ-----DSGPTF-GSMRPVY-----KITDQIDALRQIMELYIOPKX 226  
DB 318 PLEQP--TTQLCRSWYNIPARHNLNFSVLENSLIRPHELRSNQLIVN--YQING 372  
QY 227 SA-----YFWIYESDWKVRATYVNDYIGKR-----GSNTGAAMH 260  
DB 373 SAMRGSRRVRYHLSHSIIQKSKSYGLSLDPVGANINVQNNDIYQIISVSNFASPVGSSYS 432

QY 261 MWSSDPSAIYTSA---LGAAGYAPNVGV-----RYSHGGSY 294  
DB 433 VMDTN---FLLSSQVAGISGYTQGGIPAVCLQQRNSTDLEPISNPGDIIIRNYSRLSH 489  
QY 295 -----TKGMAPANTNAYAPPEFKYPGYKLSVSAVGLSKADADSVWFGFRPVLE 346  
DB 490 ITQYRFQATQSGSPSTYSANLP-----TCWTHRDVLDL 523  
QY 347 N--EANOGLDUTLALQIP-----AEIGITDVV--PAFGRTEEPINGODAIRIMESFTSGFG 397  
DB 524 NITIANQI-----TQLPLVAYELSSGATVYKGGF-----TGGDIVR--RNTGGFG 569  
QY 398 -FTYVDSPOKOKYKIYRIANMLSAS---TVSLTYNNQTFETDILNTSLDPNGRGANYG 453  
DB 570 AIRSVATGPLEQRIRIRFRYASTIDPDFVTRGGTTINFRFRTNM-----RQESRYE 624  
QY 454 SYTLVEGPI-IEFSQGNIFLQSQ---KGEPAIDSIITSPV 491  
DB 625 SYRTVEFTPEFNFQOSODIIRTSIQGLSGNGEVYLDRIEILIPV 667

RESULT 4  
US-08-880-685-2  
; Sequence 2, Application US/08880685  
; Patent No. 5834296  
; GENERAL INFORMATION:  
; APPLICANT: IIZUKA, TOSHIHIKO  
; APPLICANT: TAGAMA, MICHITO  
; APPLICANT: ARAI, SATOSHI  
; APPLICANT: MIIZEKI, MASATSUGU  
; APPLICANT: MIYAKE, TOSHIRO  
; TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL  
; TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/880,685  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/542,921  
; FILING DATE: 13-OCT-1995  
; APPLICATION NUMBER: JP 276082/94  
; FILING DATE: 14-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 49-209-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 413-3000  
; TELEFAX: (703) 413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1169 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-880-685-2

Query Match 8.7%; Score 223.5; DB 2; Length 1169;



```

APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Panitch Schwarze Jacobs & Nadel c/o A.S.
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 19930729
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-100-709-2

Query Match      8.2% Score 210.5; DB 1; Length 1167;
Beet Local Similarity 21.9%; Pred. No. 3.4e-11;
Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

QY 3 EPPSTGVITOPRIINDNFIKIAKLOFSTNOSDLOYPVLTPLRAQACWMLMLKDAT 62
DB 123 EAKSRVIDRFRILDLGLIEANIPSPRI-----IGFEVPLLSVYQANLHLALRDSV 175
QY 63 SWGQO--IDSOQLNGYAEILRLIKVTNDVNTTNOGLEKAKPLNYSDBEYLQAG 120
DB 176 -IFGERWGLTKVNDIYNROIIEIHEYSNHCVDTYNTELE----- 215
QY 121 RPDISVLRSNFKKWKMKVAKYKRGMSALSIALPFTGPBN-YPKQALKVQSRQIF 179
DB 216 -----RLGFRSLAQMRIVNQFRRELTLVLDIVALEFNVDSRLYPIQTSQLTREIVT 268
QY 180 APVIGIPGIGITSDSGPTFGSMRFDVKTYDQIDALROL-----MELYIQPLKSAFW-- 231
DB 269 SPVSEFYGVV--NSGNIIGTL-----TEQOIRRHPLMDFNMSMTMYSNDNRREHYWGL 321
QY 232 ---TY-----ESDWKVRATYVND-----YIGKR 251
DB 322 EMTAFTGPAQOVSEPLVGTGREGSAPPLTVRSVNDGIYRIISAPFYSAPFLGITVLGSR 381
QY 252 GSNLTGAAMMSSDPAIYTSALGAAGVAPNVGVYRSHSGSYTKGMANMNAVAPFEF 311
DB 382 GKPFDPALNNISPPSTIYRH--PGTVDSLVS1-----PPQNSVVP-- 421
QY 312 KPGYGLHSVSAVGLSKAPDADSVWFG--RPVLENEANOLITDIALQIPAEIGITDV 369
DB 422 -----HNGSGHRLSHVTMRASPIFHHTHSATTNTIN--PRAIIQIP-----L 464
QY 370 VAPGTEPPIINGQDAIRIWESFTSGFGT-----YVDSPOQOKXI 412
DB 465 VVAFNHLH--SGATVVR-----GPGTGDIILRTNTGTGFADNRVAVITPLSQRYAV 513
QY 413 IYRIANNIASSVSLTYVNNQTFETDILNLSLPNGVNGVGSYTLVEGIIIE----- 464

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DB 514 RIRY-----ASTDL-----QFFTRINGTSVN-----OGNF-ORITMRGNDLNSGNFRTAG 558
QY 465 -----FSQGNIFKLSQ--KGEFALDSIFSP 490
DB 559 FSTPFSFMSASTTLTGTOAFSNOEYIDRIEFV 593

RESULT 7
US-08-176-865-2
Sequence 2, Application US/08176865
Patent No. 5616319
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuying
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Panitch Schwarze Jacobs & Nadel c/o A.S.
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,865
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-176-865-2

Query Match      8.2% Score 210.5; DB 1; Length 1167;
Beet Local Similarity 21.9%; Pred. No. 3.4e-11;
Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

QY 3 EPPSTGVITOPRIINDNFIKIAKLOFSTNOSDLOYPVLTPLRAQACWMLMLKDAT 62
DB 123 EAKSRVIDRFRILDLGLIEANIPSPRI-----IGFEVPLLSVYQANLHLALRDSV 175
QY 63 SWGQO--IDSOQLNGYAEILRLIKVTNDVNTTNOGLEKAKPLNYSDBEYLQAG 120
DB 176 -IFGERWGLTKVNDIYNROIIEIHEYSNHCVDTYNTELE----- 215
QY 121 RPDISVLRSNFKKWKMKVAKYKRGMSALSIALPFTGPBN-YPKQALKVQSRQIF 179
DB 216 -----RLGFRSLAQMRIVNQFRRELTLVLDIVALEFNVDSRLYPIQTSQLTREIVT 268
QY 180 APVIGIPGIGITSDSGPTFGSMRFDVKTYDQIDALROL-----MELYIQPLKSAFW-- 231
DB 269 SPVSEFYGVV--NSGNIIGTL-----TEQOIRRHPLMDFNMSMTMYSNDNRREHYWGL 321

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Qy 232 ---IY-----ESDMKVRATVND-----YIGKR 251
Db 322 EMTAFTGTGAGAQVSEPLVGTGREGSAPPLTVRSVNDGIYRILSAPPYSAPFLGTIVLGSR 381
Qy 252 GSNTGAAMHMSDPSAIYTSALGAGYAPNVVGVVSHGSGSYTKGMAPANTNAYAPFEF 311
Db 382 GEKPDFALNNISPPSTIYRH---PGYVDSLVI-----PPDINSVP--- 421
Qy 312 KYPGYKLSVSAVYGLSKAPDAADSVMGF--RPVLLENANQLTDTALQIPAEIGITDV 369
Db 422 -----HGGSHRLSHVTMRASSPIFHTHTSATTTNTIN---PNAIIQIP-----L 464
Qy 370 VPAFGTEEPINGODAIRIWESFTSGFGFT-----YTVDSPOKOKYKI 412
Db 465 VVAFNLH---SGATVVR-----GPGFTGGDILRRITGTGFMADRVNITGFLSQRYRV 513
Qy 413 IYRIANNLSASTVSLTYNNQTFPTDILNTSLDPNGVGRNGVSYTLVSGPIIE----- 464
Db 514 RIRY-----ASTTDL-----QFTTRINGTSVN---QGNP-ORTMNRGDNLSGNFRTAG 558
Qy 465 -----FSQGTNIFKLGSQ---KGFAIDSIIIFSP 490
Db 559 FSTPFSFSAQSTFTLGTQAFSNOEYVIDRIEFPV 593

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RESULT 8
US-08-474-038-2
; Sequence 2, Application US/08474038
; Patent No. 5679343
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,038
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,865
; FILING DATE: 30-DEC-1993
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egoif, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ. ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-038-2

```

```

Query Match 8.2%; Score 210.5; DB 1; Length 1167;
Best Local Similarity 21.9%; Pred. No. 3.4e-11;
Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

Qy 3 EPPSIVGVTORPRLINDNFIKYIAKQFSTNGSDIQYPLTLPLRAQACVHMLMLKDKATT 62
Db 123 EAAKSRVIDRFRFTLIDGLLEANIIPSFRI-----IGFEVPLLSVYVQAANLHLALRDSV- 175
Qy 63 SVMGOQ--IDSQQLNGVRAELIRLIKVTNDVNTYNOGLELEKAPLNYSDPBEYLQAG 120
Db 176 -IFGERMGLTTKNVDINDYNRQIRREIHEYSNHCVDYTNLE----- 215
Qy 121 RPDISVLRSNFEVKNKRVAKYKRGMAALSIALFPPTGPN-YPPQALKVQOSROI 179
Db 216 -----RLGFRSIAQWRIYVQFRRELTLTVLIDIALFPNYSRLPYIQTFSQLTREIYV 268
Qy 180 APVIGIPGGIITSQDSGPFPGSMRPFVKYVDIDIALRQI-----MELYIQPLKSAVFW--- 231
Db 269 SFVSEFFYGVV--NSGNIIIGTL-----TEQQRPHLMDFFNSMIMYTSDNRRHHYSG 321
Qy 232 ---IY-----ESDMKVRATVND-----YIGKR 251
Db 322 EMTAFTGTGAGAQVSEPLVGTGREGSAPPLTVRSVNDGIYRILSAPPYSAPFLGTIVLGSR 381
Qy 252 GSNTGAAMHMSDPSAIYTSALGAGYAPNVVGVVSHGSGSYTKGMAPANTNAYAPFEF 311
Db 382 GEKPDFALNNISPPSTIYRH---PGYVDSLVI-----PPDINSVP--- 421
Qy 312 KYPGYKLSVSAVYGLSKAPDAADSVMGF--RPVLLENANQLTDTALQIPAEIGITDV 369
Db 422 -----HGGSHRLSHVTMRASSPIFHTHTSATTTNTIN---PNAIIQIP-----L 464
Qy 370 VPAFGTEEPINGODAIRIWESFTSGFGFT-----YTVDSPOKOKYKI 412
Db 465 VVAFNLH---SGATVVR-----GPGFTGGDILRRITGTGFMADRVNITGFLSQRYRV 513
Qy 413 IYRIANNLSASTVSLTYNNQTFPTDILNTSLDPNGVGRNGVSYTLVSGPIIE----- 464
Db 514 RIRY-----ASTTDL-----QFTTRINGTSVN---QGNP-ORTMNRGDNLSGNFRTAG 558
Qy 465 -----FSQGTNIFKLGSQ---KGFAIDSIIIFSP 490
Db 559 FSTPFSFSAQSTFTLGTQAFSNOEYVIDRIEFPV 593

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RESULT 9
US-08-779-046-2
; Sequence 2, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046

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FILING DATE: 06-JAN-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/100,709  
 FILING DATE: 29-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Egolf, Christopher  
 REGISTRATION NUMBER: 27633  
 REFERENCE/DOCKET NUMBER: 7205-49  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-757-1590  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1167 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-779-046-2

Query Match 8.2%; Score 210.5; DB 2; Length 1167;  
 Best Local Similarity 21.9%; Pred. No. 3.4e-11;  
 Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

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QY 3 EPPSTGVITOPRIINDNFYKIAKQFSTNOSDLOYPVLTPLPRAQACVMMHMLIKDATT 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 123 EAASRVIDRRIRILDGLIEANIPSPRI-----IGFEVPLLSVYQANLHLLALRDSV- 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 SVWGOQ--IDSQQLNGYKAEILIRLIKVTNDVNTTNOGLELEKAKPLNYSDBERYLOAG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 176 -IFGRMGLTTKNVNDIYNRQIREIHEYSNHCVDYNTLE----- 215
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 RPDISVLASNFEKVMKKKAKYKRGMAASLSLALFPTGPN-YPKQALKVQSRQIF 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 216 -----RLGFEPSIAQWRIYNOFRRELTLTVLDIVLPNDLSRLYPIQTSQTLREIYV 268
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 APVIGIPGIGITSODSGPFGSMRFDVKTYDQIDALROL-----MELYIQPLKSAVFW--- 231
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 269 SPVSEFYGVV--NSGNIIIGTL-----TEQDIRPHLMDFNSMIMTYSNDRREHYWGL 321
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 232 ---IY-----ESDMKVRATVYND----- 251
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 322 EMTAYFTGFAQAQVSFPLVGTGRGESAPPLTVRSVNDGIYRILSAPFYGAPFLGTIVLGSR 381
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 232 GSNTGAAMHMMSSDPSAIYTSALGAAGYAPNVGVRYSHGSGYTKGMAPANTNVAPEEF 311
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 382 GEKFDPALNNISPPSTIYRH---PGTVDSLVS-----PPODNSVPP--- 421
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 312 KYPGYKLHSVAGYLSKAPDAADSVMEGF--RPVLLNEANQLTDTALQIPAEIGITDV 369
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 422 -----HRGSSHRLSHVTMTAASSPIFHWTHRSATTNTIN---PMALIQIP-----L 464
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 370 VPAFGRTPEEPINGODAIRIMESFTSGGFT-----YTVDSPQOKYKI 412
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 465 VKAFNLH-----SGATVVR-----GPGFTGDILRRNTTGTFAADMVNVINGPLSQRYV 513
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 413 IYRIANNISASVSLTNNQTFDTDLNTSLDPNGVRKNGSYTVLVEGPPIR----- 464
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 514 RIRY-----ASTTDL-----QFTTRINGSVN-----QGNF-ORTNKGDNLESNGNFRTAG 558
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 465 -----FSQGTNIFKLGSQ--KGFPAIDSIIFSP 490
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 559 FSTPFSFSAQSTFTLGTQAFSNOEYVIDRIEFVP 593
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 10  
 US-08-881-340-2  
 Sequence 2, Application US/08881340  
 Patent No. 5942658  
 GENERAL INFORMATION:  
 APPLICANT: Donovan, William P.  
 APPLICANT: Tan, Yuding  
 APPLICANT: Jany, Christine S.  
 APPLICANT: Gonzalez Jr., Jose M.

TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5  
 TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Panlitch Schwarze Jacobs & Nadel c/o A.S.  
 ADDRESS: Nadel  
 STREET: 1601 Market Street, 36th Floor  
 CITY: Philadelphia  
 STATE: Pennsylvania  
 COUNTRY: U.S.A.

ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/881,340  
 FILING DATE: 24-JUN-1997  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/100,709  
 FILING DATE: 29-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Egolf, Christopher  
 REGISTRATION NUMBER: 27633  
 REFERENCE/DOCKET NUMBER: 7205-49  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-757-1590  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1167 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-881-340-2

Query Match 8.2%; Score 210.5; DB 2; Length 1167;  
 Best Local Similarity 21.9%; Pred. No. 3.4e-11;  
 Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

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QY 3 EPPSTGVITOPRIINDNFYKIAKQFSTNOSDLOYPVLTPLPRAQACVMMHMLIKDATT 62
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DB 123 EAASRVIDRRIRILDGLIEANIPSPRI-----IGFEVPLLSVYQANLHLLALRDSV- 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 SVWGOQ--IDSQQLNGYKAEILIRLIKVTNDVNTTNOGLELEKAKPLNYSDBERYLOAG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 176 -IFGRMGLTTKNVNDIYNRQIREIHEYSNHCVDYNTLE----- 215
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 RPDISVLASNFEKVMKKKAKYKRGMAASLSLALFPTGPN-YPKQALKVQSRQIF 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 216 -----RLGFRSIAQWRIYNOFRRELTLTVLDIVLPNDLSRLYPIQTSQTLREIYV 268
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 APVIGIPGIGITSODSGPFGSMRFDVKTYDQIDALROL-----MELYIQPLKSAVFW--- 231
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 269 SPVSEFYGVV--NSGNIIIGTL-----TEQDIRPHLMDFNSMIMTYSNDRREHYWGL 321
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 232 ---IY-----ESDMKVRATVYND----- 251
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 322 EMTAYFTGFAQAQVSFPLVGTGRGESAPPLTVRSVNDGIYRILSAPFYGAPFLGTIVLGSR 381
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 232 GSNTGAAMHMMSSDPSAIYTSALGAAGYAPNVGVRYSHGSGYTKGMAPANTNVAPEEF 311
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 382 GEKFDPALNNISPPSTIYRH---PGTVDSLVS-----PPODNSVPP--- 421
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 312 KYPGYKLHSVAGYLSKAPDAADSVMEGF--RPVLLNEANQLTDTALQIPAEIGITDV 369
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 422 -----HRGSSHRLSHVTMTAASSPIFHWTHRSATTNTIN---PMALIQIP-----L 464
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 370 VPAFGRTPEEPINGODAIRIMESFTSGGFT-----YTVDSPQOKYKI 412
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 465 VKAFNLH-----SGATVVR-----GPGFTGDILRRNTTGTFAADMVNVINGPLSQRYV 513
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 413 IYRIANNLSASTVSLTYNNQTEFTDILNTSLDPNGVGVGYTLVEGP1IE----- 464  
DB 514 RIRY-----ASTTDL-----QFTTRNGTSVN-----QGNF-QRTMRGDNLSGNFRTAG 558  
QY 465 -----FSQGTNIFKLGSO---KGEPAIDSIIFSP 490  
DB 559 FSTPFSFSAQSTFTLGTQAFSNOQEVYIDRIEVP 593

RESULT 11  
US-08-291-368-4  
Sequence 4, Application US/08291368  
Patent No. 5686069  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel M.  
APPLICANT: Sick, August J.  
TITLE OF INVENTION: No. 5686069e1 Bacillus thuringiensis Isolates  
TITLE OF INVENTION: Active Against Lepidopteran Pests  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/291,368  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/597,607  
FILING DATE: 15-OCT-90  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: MASO.C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904)375-8100  
TELEFAX: (904)372-5800  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1168 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: BACILLUS THURINGIENSIS  
STRAIN: Morrisoni  
INDIVIDUAL ISOLATE: PS91C2  
IMMEDIATE SOURCE:  
LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF TERESA  
LIBRARY: THOMPSON  
CLONE: 91C2  
US-08-291-368-4

Query Match 8.1%; Score 207.5; DB 1; Length 1168;  
Best local Similarity 22.7%; Pred. No. 6.8e-11;  
Matches 131; Conservative 77; Mismatches 200; Indels 169; Gaps 30;  
QY 10 ITQFRILNFIYIAKL-QFSTNOSDLQ-----YPVL 41  
DB 95 ITTLRGLASVYEVLLALAKREWMENPNNAQURQREDVRIRPANTDALITAINFTLISFEIP 154

QY 42 TLPLBAQCWHEMLKXDATTWVGQIQISQGLNGYAKELRLIKVYNDVNTFYNOGLE 101  
DB 155 LLSVYQANILSLILKRAVSPGQGWGIDITVNNHNRLLNLHRYHEHCLDTYNOGLE 214  
QY 102 LEKAKPLNYSDBEEYLAQRBDISLRSPNFKVKKWNAKYKGMASALSALAPPTF 161  
DB 215 -----NLRGNTNQ-----MSRFNGFRRLTLTVLDIYALFPNY 248  
QY 162 GPN-YPKQALKVVSQRIF-----APV-IGIRGITSQSGPFGSMRDYKTYDID 212  
DB 249 DARAYPIQTSSQL-TREIYTSVIEDSPSANIPNG-----FNRAEFGVRPPLMD 298  
QY 213 ALRQIMELYIOLPSAYFW--IYESDMKVRATYNDYIGKGSNTGAAMHMSDPSAIY 270  
DB 299 FWNLSLF-VTAETVNSQTYGCHLYSRRNTAGNPINFPYGVNPGALIW-IADEDDPRPFY 356  
QY 271 TS-----ALGAGYAPNVVGV---YSHGSGYTKG-----APANTVAAPF 309  
DB 357 RLSDPVPVVRGPGPHVLGLRGVFGQGTGNTNRTFRNSGTIDSLDEIPPODSGAPW 416  
QY 310 E-----FKYPGYKLHSVSAVGLSKAPDAADSVFGEFRPVLLNENAOILLTAL 358  
DB 417 NDYSHVLNHTVFRWPG---EIGSDSWRAP-----MFSWTH-RSADRTNIINPNIT 465  
QY 359 QIPA-----EIGITDV-VPAQRTEEPINGODAIRIWESFTSGHG-FTYTVDSPOKXY 410  
DB 466 QIPAVKANHLSGSTVVGPGP-----TGADLRL-RNYTGTFADIRVNTITGPLSORY 516  
QY 411 KIYRIANNLSASTVSLTYNNQTEFTDILNTSLDPNGVGVGYTLVEGP1IE----- 464  
DB 517 RYRIY-----ASTTDL-----QFTTRNGTSVN-----QGNF-QRTMRGDNLSGNFRT 561  
QY 465 -----FSQGTNIFKLGSO---KGEPAIDSIIFSP 490  
DB 562 AGFSTPFSFSAQSTFTLGTQAFSNOQEVYIDRIEVP 598

RESULT 12  
US-08-962-190-4  
Sequence 4, Application US/08962190  
Patent No. 5985267  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel M.  
APPLICANT: Sick, August J.  
TITLE OF INVENTION: No. 5985267e1 Bacillus thuringiensis Isolates  
TITLE OF INVENTION: Active Against Lepidopteran Pests  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: US  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/962,190  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/291,368  
FILING DATE:  
APPLICATION NUMBER: 07/597,607  
FILING DATE: 15-OCT-90  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: MASO.C1  
TELECOMMUNICATION INFORMATION:



TELEPHONE: (904)375-8100  
 TELEFAX: (904)372-5800  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1168 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHEICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: BACILLUS THURINGIENSIS  
 STRAIN: Morriisoni  
 INDIVIDUAL ISOLATE: PS91C2  
 IMMEDIATE SOURCE:  
 LIBRARY: LAMBDAGEN (TM) - 11 LIBRARY OF TERESA  
 LIBRARY: THOMPSON  
 CLONE: 91C2  
 US-08-962-190-4

Query Match 8.1%; Score 207.5; DB 2; Length 1168;  
 Best Local Similarity 22.7%; Pred. No. 6.8e-11;  
 Matches 131; Conservative 77; Mismatches 200; Indels 169; Gaps 30;

QY 10 ITQRIINDNFIKTYAKL-QFSTNQSIDIQ-----YFVL 41  
 DB 95 ITTLGLADSEYVLEALREWEENPNNAQLREVRIRPANTDDALITAINNFTLTSFEIP 154  
 QY 42 TLPLRAQCVHMLMLDKATTSVWGQIDSOQLNGYKAEILRLIKVYNDVNTYNOGLE 101  
 DB 155 LLSVYVQANLHLILRLDAVSFGQGWGIDIAVNNHYNRLNLHRYTEHCLDTYNOGLE 214  
 QY 102 LEKAKPLNYSDEEYLQGRPDISVLSNFKKVMKMKVAKYKGMASALSIALPPTF 161  
 DB 215 -----NLRGNTNRQ---MSRFNQFRRLTLTVLDIYALFPNY 248  
 QY 162 GPN-YPKQALKVVSROIF-----APV-IGIPGITSQDSGPTFGSMRDPVKTYYDID 212  
 DB 249 DARAVPIQTSSQL-TREIYTSVIEDSPVSANIPNG-----FNRAEFGVPRPHLMD 298  
 QY 213 ALRQIMELIYIOLKSAVFW--IYESDMKVRATYNDYIGKSGNTGAAMHMSDPSAIY 270  
 DB 299 FPNLSLF-VTAETVRKQTYWGHVLSKRTAGNPIFPIYGVNPGGALN-INDDEPRREFY 356  
 QY 271 TS-----ALGAAGYAPNVVGR---YSHGGSYTKM-----APANTVAAPF 309  
 DB 357 RLISDPVFGGFGDPHYVLGLRGVFOQTGNTNHTRTFRNSGTIDSLDEIPQDNGAPW 416  
 QY 310 E-----FKYPGKLSVSAVGLSKAPDAADSVFGRPVLLERENQILITDAL 358  
 DB 417 NDYSHVNLHVTFFVRWFG---ELAGSDSWRAP-----MFSWTH-RSADRTMIINPNIT 465  
 QY 359 QIPA-----EIGITDV-VPAFGTEBPINGODAIRIMESFTSGHG-FTYTVDSPOKQY 410  
 DB 466 QIPAVKANHLMSGSTVVRGPGF-----TGGLDLR-RTNTGTADIRVNTITGGLSQRY 516  
 QY 411 KLIYRIANNLSASTVSLTYNNQTFETDILNLSLDPNGVAGNYSYLVGPIIE----- 464  
 DB 517 RYRIYV-----ASTTDL-----QFETRLINGTSVN-----QGNF-QSTNRGMDLESNGNPT 561  
 QY 465 -----FSQGTINIFKQSQ--KGEFAYDSITISP 490  
 DB 562 AGFTSPFSFSAQSTFTLGTQAFSNOEYVIDRIEFPV 598

RESULT 13  
 PCT-US95-10310-4  
 Sequence 4, Application PC/TUS9510310  
 GENERAL INFORMATION:  
 APPLICANT: MYCOGEN CORPORATION  
 APPLICANT: STREET ADDRESS 5501 Oberlin Drive  
 APPLICANT: CITY: San Diego

APPLICANT: STATE/PROVINCE: California  
 APPLICANT: COUNTRY: US  
 APPLICANT: POSTAL CODE/ZIP: 92121  
 APPLICANT: PHONE NUMBER: (619) 453-8030  
 APPLICANT: FAX NUMBER: (619) 453-6991  
 TITLE OF INVENTION: Protein Toxins Active Against Lepidopteran Pests  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Saliwanhik & Saliwanhik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL  
 COUNTRY: US  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/10310  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/597,607  
 FILING DATE: 15-OCT-90  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanhik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: MA50.C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (904)375-8100  
 TELEFAX: (904)372-5800  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1168 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHEICAL: YES  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: BACILLUS THURINGIENSIS  
 STRAIN: Morriisoni  
 INDIVIDUAL ISOLATE: PS91C2  
 IMMEDIATE SOURCE:  
 LIBRARY: LAMBDAGEN (TM) - 11 LIBRARY OF TERESA  
 LIBRARY: THOMPSON  
 CLONE: 91C2  
 PCT-US95-10310-4

Query Match 8.1%; Score 207.5; DB 5; Length 1168;  
 Best Local Similarity 22.7%; Pred. No. 6.8e-11;  
 Matches 131; Conservative 77; Mismatches 200; Indels 169; Gaps 30;

QY 10 ITQRIINDNFIKTYAKL-QFSTNQSIDIQ-----YFVL 41  
 DB 95 ITTLGLADSEYVLEALREWEENPNNAQLREVRIRPANTDDALITAINNFTLTSFEIP 154  
 QY 42 TLPLRAQCVHMLMLDKATTSVWGQIDSOQLNGYKAEILRLIKVYNDVNTYNOGLE 101  
 DB 155 LLSVYVQANLHLILRLDAVSFGQGWGIDIAVNNHYNRLNLHRYTEHCLDTYNOGLE 214  
 QY 102 LEKAKPLNYSDEEYLQGRPDISVLSNFKKVMKMKVAKYKGMASALSIALPPTF 161  
 DB 215 -----NLRGNTNRQ---MSRFNQFRRLTLTVLDIYALFPNY 248  
 QY 162 GPN-YPKQALKVVSROIF-----APV-IGIPGITSQDSGPTFGSMRDPVKTYYDID 212  
 DB 249 DARAVPIQTSSQL-TREIYTSVIEDSPVSANIPNG-----FNRAEFGVPRPHLMD 298

QY 213 ALRQIMELXIOPKSAVFW--IYESDWKVRATVYNDYIGKSGNTGAAHMMSSDPSAIY 270  
DB 299 FMNSLIF-VTAETVRS-----QIYWGGHLVSSRNTAGRINFPBGVFNPGGAIWIADDED 351  
QY 271 TS-----ALGAGYAPNVVGR---YSHGGSYTKGM-----APANTYAYAPF 309  
DB 357 RLSDPVPFRGGGDPDHVYLGLRGVGFQQTGNNHTRTFPNSGRTISDLDEIPQDNGANW 416  
QY 310 E-----FKYPGYKLHSVSAVGLSKAPPAADSVMPGFRPVLLNEANQLLTOTAL 358  
DB 417 NDYSHVHNHTVFRWPG---EISGDSWRAP-----MFSWTH-RSADRTMIINPNTI 465  
QY 359 QIPA-----EIGITDV-VPAGRTTEPINGODAIRIMESFTSGEG-FTYTVDSPQKXY 410  
DB 466 QIPAYKANHLHSGSYVGRGPF-----TGDDLK-RRTNGTFADIRIVNTIGPLSQRY 516  
QY 411 KIIRYIANNLSASTVSLTYNNQTFPTDIINTSLDPNGVGNYSYLVGEPPIE----- 464  
DB 517 RVRIRY-----ASTIDL-----QFFRINTGSYN---QGNF-QRTMANGDNLESQNPRT 561  
QY 465 -----FSOGTNIKLGSO--KGEPAIDSIIESP 490  
DB 562 AGSTPFSFMSAQSTFTLGTQAFSNQEVYIDRIEFVP 598

RESULT 14  
US-09-178-252-4  
; Sequence 4, Application US/09178252  
; Patent No. 6218188  
; GENERAL INFORMATION:  
; APPLICANT: Cardineau, Guy A.  
; APPLICANT: Navea, Steven J.  
; APPLICANT: Navea, Kenneth E.  
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
; FILE REFERENCE: MA-714XC2  
; CURRENT APPLICATION NUMBER: US/09/178,252  
; PRIOR FILING DATE: 1998-10-23  
; EARLIER APPLICATION NUMBER: 60/065,215  
; PRIOR FILING DATE: 1997-11-12  
; EARLIER APPLICATION NUMBER: 60/076,445  
; PRIOR FILING DATE: 1998-03-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 605  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
US-09-178-252-4

Query Match 7.8%; Score 200; DB 3; Length 605;  
Best Local Similarity 22.0%; Pred. No. 1.3e-10;  
Matches 127; Conservative 79; Mismatches 204; Indels 168; Gaps 29;  
QY 10 ITQFRLINDNFIKYIAKL-QFSTNOSDLO-----YPLV 41  
DB 95 ITTLRLASLSEYIYIALREWEANPNNAQLREDAVRIRPANTDDALITAINNFTLTSFIRP 154  
QY 42 TLPLRAQACVMHMLLKDATTSVWGQOISQOLNGYKAEILIRLIKVTYNDVNTYNOGLE 101  
DB 155 LLSVYQAAANHLSLRLADAVSFGQGWGLDIATVNNHNYRLINLIHRYTKHCLDITYNOGLE 214  
QY 102 LEKAKPLNYSDEPEYLAQGRPDISVLRSNFKEVWKNNKVAKYKQGMASALSIALPPTF 161  
DB 215 -----NLRGNTNRQ---WARFNQFRRLDTLTLVDIYALFPNY 248  
QY 162 G-PNYPKQALKVVSQRIQF-----APV-IGIPGIGTSQDSGPTGSMRFDVYKTYDQID 212  
DB 249 DVRTYPIQTSQOL-TREIYTSVIEDSPVSANIPNG-----FNRAEFGVRPPLHMD 298  
QY 213 ALRQIMELXIOPKSAVFWIYESDWKVRATVYNDYIGKSGS-----NTGAAMHMMSSD 265

DB 299 FMNSLIF-VTAETVRS-----QIYWGGHLVSSRNTAGRINFPBGVFNPGGAIWIADDED 351  
QY 266 PSAIYTS-----ALGAGYAPNVVGR---YSHGGSYTKGM-----APANTN 304  
DB 352 PRPFYRLSDPVPFRGGGDPDHVYLGLRGVAFQQTGNNHTRTFPNSGRTISDLDEIPQD 411  
QY 305 AYAPE-----FKYPGYKLHSVSAVGLSKAPPAADSVMPGFRPVLLNEANQL 353  
DB 412 SGAPWNDYSHVHNHTVFRWPG---EISGDSWRAP-----MFSWTH-RSADRTMIID 460  
QY 354 TDTALQIP-----AIGITDV-VPAGRTTEPINGODAIRIMESFTSGEGFTYTIV----- 402  
DB 461 PERIQLIPLVKAHLIQTGTYVGRGPF-----TGDDLK-----RTSGGFAYTIYVIN 509  
QY 403 -DSPQKQKRYKIIRYIANNLSASTVSLTYNNQTFPTDIINTSLDPNGVGNYSYLVGEPPIE----- 455  
DB 510 GOLPQRYARARIRYASTNL---RIYVTVAGERIRFAGCFNKMTD-TGDELTFQSFSEYATIN 565  
QY 456 TLVEGPIIE--FSOGTNIKLGSOKEPAIDSIIESPV 491  
DB 566 TATTFPMSQSFYVAGADTFSSGN--EYIDRFELIYV 600

RESULT 15  
US-09-826-660-4  
; Sequence 4, Application US/09826660  
; Patent No. 6673990  
; GENERAL INFORMATION:  
; APPLICANT: Cardineau, Guy A.  
; APPLICANT: Steiman, Steven J.  
; APPLICANT: Navea, Kenneth E.  
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins  
; FILE REFERENCE: MA-714XC2D1  
; CURRENT APPLICATION NUMBER: US/09/826,660  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 09/178,252  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: 60/065,215  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/076,445  
; PRIOR FILING DATE: 1998-03-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 605  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene  
US-09-826-660-4

Query Match 7.8%; Score 200; DB 4; Length 605;  
Best Local Similarity 22.0%; Pred. No. 1.3e-10;  
Matches 127; Conservative 79; Mismatches 204; Indels 168; Gaps 29;  
QY 10 ITQFRLINDNFIKYIAKL-QFSTNOSDLO-----YPLV 41  
DB 95 ITTLGLADSEYIYIALREWEANPNNAQLREDAVRIRPANTDDALITAINNFTLTSFIRP 154  
QY 42 TLPLRAQACVMHMLLKDATTSVWGQOISQOLNGYKAEILIRLIKVTYNDVNTYNOGLE 101  
DB 155 LLSVYQAAANHLSLRLADAVSFGQGWGLDIATVNNHNYRLINLIHRYTKHCLDITYNOGLE 214  
QY 102 LEKAKPLNYSDEPEYLAQGRPDISVLRSNFKEVWKNNKVAKYKQGMASALSIALPPTF 161  
DB 215 -----NLRGNTNRQ---WARFNQFRRLDTLTLVDIYALFPNY 248  
QY 162 G-PNYPKQALKVVSQRIQF-----APV-IGIPGIGTSQDSGPTGSMRFDVYKTYDQID 212  
DB 249 DVRTYPIQTSQOL-TREIYTSVIEDSPVSANIPNG-----FNRAEFGVRPPLHMD 298  
QY 213 ALRQIMELXIOPKSAVFWIYESDWKVRATVYNDYIGKSGS-----NTGAAMHMMSSD 265

```

Db 299 FMNSLF-VTAETVRS-----QVWGHIVSSRNTAGNRINFPsyGVNPGAIWIADDED 351
QY 266 PSAIYTS-----ALGAGYAPNVVGV-----YSHGGSYTKGM-----APANTN 304
Db 352 PRPFYRTLSDPVFRGFGFNPHYVLGLRGVAFQOTGTHNTRIFPNNSGTIISLDEIIPODN 411
QY 305 AYAPPE-----FKYPGYKLSVSAVGLSKAPDAADVWFGFPPVLLNEANQIL 353
Db 412 SGAPWMDYSHVNLNHTFVRWFG-----EISGSDSWRAF-----MFSWTH-RSATPTNTID 460
QY 354 TDTALQIP-----AEIGITDV-VPAFGRTPEEPINGODAIRIWESFTSGFGFTYTV----- 402
Db 461 PERITQIPLVKAHTLOSSTTVRGPGF-----TGCDILR-----RTGGPFAYTIVIN 509
QY 403 -DSPQKQYKXIIYRIANNLSASTVSLTYNNQTFFTDILNTSIDPVGVRNGVSY----- 455
Db 510 GOLPORRYRIRRYASTNL--RIYTVAGERIFAGQFNKTMD-TGDPITFOSFSYATIN 565
QY 456 TLVEGPPIE--FSOGTNIFFKLGSOKGEPAIDSIIPSPV 491
Db 566 TAFTEPMQSSFTVGADTFSSGN--EYIDRFELIPV 600

```

Search completed: October 19, 2005, 20:19:21  
 Job time : 46 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 19, 2005, 20:04:21 ; Search time 166 Seconds  
(without alignments)  
1146.302 Million cell updates/sec

Title: US-10-756-778-8  
Perfect score: 2560  
Sequence: 1 IAEPPSTGVITQFRLNDNF.....KLGSKQKEFAIDSIIFSPV 492

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	9.0	825	ADP43080	Adf43080 Bacillus
2	228.5	8.9	1138	AAR06461	Aar06461 BtPGS1245
3	228.5	8.9	1138	ADR89429	Adr89429 cry7Aa.1
4	227.5	8.9	1152	AAB84630	Aab84630 Amino aci
5	225.5	8.8	1138	AAR37213	Aar37213 B.t. toxi
6	224.5	8.8	1138	AAR46225	Aar46225 Bacillus
7	223.5	8.7	1169	AAR6126	Aar6126 Bacillus
8	222.5	8.7	1138	AAR46226	Aar46226 Bacillus
9	220.5	8.6	1138	AAR37214	Aar37214 B.t. toxi
10	214	8.4	1186	AAU00419	Aau00419 Bacillus
11	210.5	8.2	1167	AAR54073	Aar54073 CryET4. 2
12	210.5	8.2	1167	AAW5258	Aaw5258 Bacillus
13	210.5	8.2	1167	AAW17700	Aaw17700 CryET4. 3
14	210.5	8.2	1167	AAW87632	Aaw87632 CryET4 pr
15	210.5	8.2	1167	AAW30922	Aaw30922 B. thurin
16	207.5	8.1	1168	AAR89493	Aar89493 CryIF cia
17	207	8.1	1168	ADR9437	Adr9437 Cry39Aa.
18	203	7.9	1174	AAR94916	Aar94916 Native Cr
19	201	7.9	1157	AAW84581	Aaw84581 Amino aci
20	201	7.9	1157	AAW84583	Aaw84583 Amino aci
21	201	7.9	1157	AAW84591	Aaw84591 Amino aci
22	200	7.8	605	AAW16791	Aaw16791 Truncated
23	200	7.8	605	AAU00532	Aau00532 Truncated
24	200	7.8	718	AAW61024	Aaw61024 Chimeric
25	200	7.8	1148	AAR84733	Aar84733 CryIF/cry

26	200	7.8	1148	2	AAR84731	Aar84731 CryIF/cry
27	200	7.8	1148	2	AAR94907	Aar94907 CryIF/cry
28	200	7.8	1148	2	AAW76709	Aaw76709 Plasmid p
29	200	7.8	1148	2	AAW76715	Aaw76715 Consensus
30	200	7.8	1148	2	AAW76718	Aaw76718 Alternati
31	200	7.8	1148	2	AAW76717	Aaw76717 Alternati
32	200	7.8	1148	2	AAW76707	Aaw76707 Plasmid p
33	200	7.8	1148	2	AAW16790	Aaw16790 Plant-opt
34	200	7.8	1148	4	AAU00531	Aau00531 CryIF/cry
35	200	7.8	1157	2	AAW84569	Aaw84569 Amino aci
36	200	7.8	1174	2	AAR10131	Aar10131 Lepidopte
37	200	7.8	1174	2	AAR14856	Aar14856 CryIF pro
38	200	7.8	1174	2	AAR39754	Aar39754 Delta end
39	200	7.8	1174	2	AAR84732	Aar84732 CryIF/436
40	200	7.8	1174	2	AAR84735	Aar84735 CryIF tox
41	200	7.8	1174	2	AAR94908	Aar94908 CryIF/436
42	200	7.8	1174	2	AAR94914	Aar94914 CryIF tox
43	200	7.8	1174	2	AAW76712	Aaw76712 B. thurin
44	200	7.8	1174	2	AAW76710	Aaw76710 Plasmid p
45	200	7.8	1174	2	AAW76708	Aaw76708 Plasmid p

## ALIGNMENTS

RESULT 1	ADP43080	standard; protein, 825 AA.
ID	ADP43080	
XX	ADP43080	
AC	ADP43080	
XX	ADP43080	
DT	12-FEB-2004	(first entry)
XX		
DE	Bacillus thuringiensis toxin protein sequence.	
XX		
KW	cell recognition; cell-damaging; cytostatic; anticancer;	
KM	cancer affected cell.	
XX		
OS	Bacillus thuringiensis.	
XX		
FN	JP200310277-A.	
XX		
PD	05-NOV-2003.	
XX		
PF	30-APR-2002; 2002JP-00129344.	
XX		
PR	30-APR-2002; 2002JP-00129344.	
XX		
PA	(FUKU-) FUKUOKA KEN.	
XX		
DR	WPI, 2004-027149/03.	
DR	N-PSDB; ADP43079.	
XX		
PT	Novel polynucleotide encoding a 88 kDa protein having cell	
XX	recognizing/cell damaging activity useful as an anticancer agent.	
PS	Claim 15; SEQ ID NO 2; 26pp; Japanese.	
XX		
CC	This invention relates to a novel nucleotide with specific cell	
CC	recognizing and cell-damaging activity. The invention may be useful for	
CC	the development of compositions with a cytostatic (anticancer) activity	
CC	which damages cancer affected cells.	
XX		
SQ	Sequence 825 AA;	
XX		
Query Match	9.0%; Score 230; DB 8; Length 825;	
Best Local Similarity	21.0%; Pred. No. 1.8e-11;	
Matches	120; Conservative 90; Mismatches 213; Indels 148; Gaps 24;	
QY	9 VITGRRIN--DNFIKIALQFSTNOSDIQYPLTIPLAQAQCVHMLIKQATT--S 63	
DB	164 VLTERRVNGHFENSMPSFAVRNFEVN-----LLPVYAERANLHLIRDAVKFGE 214	

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QY 64 VMGQID--SQOLNGYKAEILRLIKYTNVDVNTTNOGLELEKAKPLNYSDBE-----BY 116
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 215 GWMSTDPGEARDDMYR-RLRSRTETIYDHCVTYNOGLQAKSLQANVSDRSRYPMWY 273
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 117 LQAGRPDISVLSNFEWKKMKVAKYKKGMMASLSLALPPTPEPNPKQALKVQSR 176
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 274 NQSGGSEYBAAGEYKGTENMNLNNAFRKDMTLVLIDIAQFPPTYDPGLYSRPVSELR 333
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 177 QIFAPVIGIPGIGITSQDSGPTFGSMRFDVKTVDQID---ALROL-----MELYIOP 224
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 334 EYVYTDIRG-----TWRSQANLNTIDALENRWVSRQLQFLTWLEMKYIYN 381
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 225 LKSAFWIYES---DMKVRATYVND-YIGKSGNTGA-----WH-----260
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 382 TCSITSYTHGDLVWGLEKKIRKTNDDQWLPLEGQNTSYTRIDRPGIELEKMYVYARQ 441
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 261 -----MM-SSDPSAIYTSALGAGYAPNVVGRYHGGSYTGMAAPATNVAPE 310
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 442 QMFETRLLOLMANTDVLNAGTVGNEFWVRDVPDRNTYASTRNHFTENHRLSWIKPE 501
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 311 -----FKYPGYKLHSVSAVGLSKAPDAADSVMFGRPVLLNEANQLLDTALQIPA- 362
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 502 PYRDNCFAMPGYKQSLALFGWTNNSVDLNNIISQYR-----ITQIPAV 546
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 363 ---EIGITDVPAFGRTTEPINGODAIRIMESFTSGFGFTYTVDSPOKOKYKIIRAN 418
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 547 KAYMNRGAFSVIRGPST---GGNLVQL-----GTGGEVSVKVRPEQTSQDWYRARI 595
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 419 NLSAST-----VSLTYN-NOTFFTLDIANTSLDNGVRGNGSYTIVBGP 463
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 596 RFAAGSRGLNKKYVSSIHASTYTDYNNMTM-----SSSTQGTVNSFOYLD--VY 643
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 464 EFSOGTNIIFKL--GSQKGEFAIDSIIFSPV 491
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 644 NFRLAPEFEVWLNTNESGPIWIDKIEFTPL 674
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 2
AAR06461
ID AAR06461 standard; protein; 1138 AA.
XX
AC AAR06461;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 03-JAN-1991 (first entry)
XX
DE BtPGS1245 protoxin.
XX
XX Toxin; crystal; insecticide.
XX
XX Bacillus thuringiensis; strain PGs1245.
OS
FH Key Location/Qualifiers
FT Protein /label= BtPGS1245
XX
XX EP382990-A.
XX
XX 22-AUG-1990.
XX
XX 15-FEB-1989; 89EP-00400428.
XX
XX 15-FEB-1989; 89EP-00400428.
XX
XX 15-FEB-1989; 89EP-00400428.
XX
XX (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
XX Peferoen M, Lambert B, Joos H;
XX
XX WPI; 1990-255362/34.
XX
XX N-PSDB; AAG05680.
XX
XX New Bacillus thuringiensis strains - producing toxin active against
PT

```

```

PT Coleoptera.
XX
XX Claim 2; Fig 2; 30pp; English.
XX
CC The BtPGS1245 strain was isolated from grain dust and was deposited at
CC the DSM (19/1/1989) under Acc. No. 5132. The protoxin (129 kD) can be
CC digested with trypsin to produce the mature protein (66 kD). The proteins
CC formed during sporulation are packaged in bipyramidal crystals. Plants
CC contg. the gene encoding the toxin are resistant to Coleoptera pests
CC while the crystals are useful as insecticides. The gene can also be
CC truncated and used to produce chimaeric genes together with the bPGS1208
CC gene (AAG05679). See also AAR06460. (Updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 1138 AA;

Query Match      8.9%; Score 228.5; DB 2; Length 1138;
Best Local Similarity 22.4%; Pred. No. 4.1e-11;
Matches 124; Conservative 70; Mismatches 216; Indels 143; Gaps 23;

QY 9 VITOPRINDNFIKXIYIAKLOFTNSQSDIQ-YPVLTLPRAQACVHMLMDATT--SVW 65
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 157 VATERRIIDSLF-----EFSMPSFKYTGIEIPLLTYAQAANLHLALDSTLYGDKW 209
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 66 G--QOIDSQOLNGYKAEILRLIKYTNVDVNTTNOGLELEKAKPLNYSDBEYIQAQRPD 123
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 210 GFTQNNIENYNRQK---KRISEYSDHCTKWNSGLS-----243
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 124 ISVLSNKEVKKMKVAKYKKGMMASLSLALPPTGPNPKQALKVQSRQIFAVI 183
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 244 ---RLNSTYEQWLNINFRREMILMALDLVAVFPFHDPRYSMETSTOLREYVTDV 299
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 184 GIPGIGITSQDSGPTFGSM-RFDVKTVDQIDALROLMELYIQPLKSAFWIYESDVKVRAT 242
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 300 SL--SISNPDIQSPESQMENTAIRPHLVYLDL-----YITTSKTKASH 344
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 243 YVNDYIGKSGNTGAHMTMS-----SDPSAIYTSAL--GAAGYAPNVVGRYSHGG 292
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 345 EIQPDL-----FYMSAHKVSFKKSEQSNLYTTGIGIKTSGYISS--GAYSFHGN 391
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 293 SYTKGMAPANTNAYAPFEFKYR---GYKLHSVSAVGL-----SKAPDAADSVW 337
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 392 DIYRTLA-----APSVVVPYTONVGEQVEFYGAVGHVHRGDNKYDLTYPSIDQLP 444
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 338 FGFRPVLLNEANQLLDTALQIPAIEIGITDVPAFGRT-----EPINGODAI 386
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 445 PDGEPI-HEKTYHRLCHATAIFKSTPYDNAATTIPFSWTHSAEYRNIRYPNKTIKIPAV 503
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 387 RIWE-----SFTSGFGFT-----YTVDSPOKOKYKIIRANLSAST 424
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 504 KMYKLDDESTVVKGGFTGDLVKRSGTYIGDIKATVNSPLSQKYRVRVAVATVSGQF 563
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 425 VSLTYNNOTFFTLDIANT-SLDPNGVRGNGSYTIVE-GPIIEFSOGTNIIFKLG-----SQK 478
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 564 NVYINDKTLITQKQNTVETIGEGKDLTYGSGFYIEYSTTIOFPDEHPKTIHLSDLNN 623
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 479 GEPFADSIIFSPV 491
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 624 SSFYVDSIEFTIPV 636
XX |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 3
ADR89429
ID ADR89429 standard; protein; 1138 AA.
XX
AC ADR89429;
XX
DT 18-NOV-2004 (first entry)
XX
XX cry7Aa.
XX
XX delta-endotoxin; delta-endotoxin associate polypeptide;
XX expression cassette; transformation; transgenic; plant; bacteria;
KW

```

KW	lepidoptera; coleoptera; pest; pesticide; resistance;
KM	pesticidal activity.
XX	
OS	Bacillus thuringiensis.
PN	MO2004074462-A2.
XX	
PD	02-SEP-2004.
XX	
PF	20-FEB-2004; 2004WO-US005829.
XX	
PR	20-FEB-2003; 2003US-0448632P.
PR	20-FEB-2003; 2003US-0448633P.
PR	20-FEB-2003; 2003US-0448797P.
PR	20-FEB-2003; 2003US-0448806P.
PR	20-FEB-2003; 2003US-0448810P.
PR	20-FEB-2003; 2003US-0448812P.
PR	19-FEB-2004; 2004US-00781979.
PR	19-FEB-2004; 2004US-00782020.
PR	19-FEB-2004; 2004US-00782096.
PR	19-FEB-2004; 2004US-00782141.
PR	19-FEB-2004; 2004US-00782570.
PR	19-FEB-2004; 2004US-00783417.
XX	
PA	(ATHE-) ATHENIX CORP.
XX	
PI	Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;
XX	
DR	WPI; 2004-635574/61.
XX	
PT	New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids
PT	and polypeptides, useful for killing lepidopteran or coleopteran pests or
PT	for producing organisms with pesticide resistance.
XX	
PS	Example 6; SEQ ID NO 41; 178bp; English.
XX	
CC	This sequence represents a delta-endotoxin crystal protein. This protein
CC	was included in the scope of the invention as a comparison to the delta-
CC	endotoxins of the invention. Some of the delta-endotoxin coding sequences
CC	of the invention have alternative start codons, producing more than one
CC	protein from a single open reading frame. The nucleic acid sequences of
CC	the invention are useful in DNA constructs or expression cassettes for
CC	transformation and expression in plants and bacteria. The nucleic acids
CC	and corresponding polypeptides are useful for killing lepidopteran or
CC	coleopteran pests. Compositions containing the delta-endotoxins of the
CC	invention, and methods for their production, are useful for the
CC	production of organisms with pesticide resistance, specifically bacteria
CC	and plants. These organisms are useful for generating altered or improved
CC	delta-endotoxin or delta-endotoxin-associated proteins that have
CC	pesticidal activity, or for detecting the presence of delta-endotoxin or
CC	delta-endotoxin-associated proteins or nucleic acids in products or
CC	organisms.
XX	
SQ	Sequence 1138 AA;
XX	
Query Match	8.9%; Score 228.5; DB 8; Length 1138;
Best Local Similarity	22.4%; Pred. No. 4,1e-11;
Matches 124; Conservative	70; Mismatches 216; Indels 143; Gaps 23
QY	9 VITGRIILNDFIKYIAKIQSTNSDLO-YPLVITPLPRAQCVWHMLLKDATT--SVW 65
DB	157 VATERRIIDSLF-----EFSGMPSEKVGYEIPLLTVYAQAANLHALLRSDTVGDKW 209
QY	66 G--QQIDSQLNGYKAEILRIKLVYNDVNTYTNOSGLEKKAKPLNYSPEEVLQAGRDP 123
DB	210 GTTQNNIENYRQK---KRISVSDHCKTKMNSLS----- 243
QY	124 ISVLRSNFKFEVWKWNVAKYKRGKGMASLSLALPFTFGPNYPKQALKVYOSRQIFAPYI 183
DB	244 ----RNGSTYSGWIMVYNNFRREMLIMALDIVAVPFPHDPRRYSMETSQTQLREVYTDVP 299
QY	184 GIPGGITSDSGPFGSM-RFDVKYTDQIDALRQLMELYIQPLKSAFYMYIESDMKVRAT 242

Query	Match	8.9%	Score 227.5	DB 4	Length 1152
Db	300 SL--SISNPDIQSPFSQMENTAIFRPHLVDYDEL-----YIYSKYAFSH 344				
Qy	243 YVNDYIGKRGSGNTGAAMHMS-----SDPSAIYTSAL--GAAGYARNVGVRSHG 292				
Db	345 EIQPDL-----FYMSAHKVSFKKSEQSNLYTTGIYKGTSGYISS--GAYSFHGN 391				
Qy	293 SYTKMAPANTNAVAPFEFKYP---GYKLHVSAYGL-----SKAPDADSVM 337				
Db	392 DIYRFLA-----APSVVVYPTTONGYGEQVEFGVKHVRHNGNKTDLTYSIDQLP 444				
Qy	338 FGFRFVLLLENANQLLDTALQIPAEIGITDVPAFGRT-----EPINGQDAI 386				
Db	445 PDGEEI-HEKYNHRCCHATAIFKSPDPYDNATIPFSWTHRSAEYNNRYPNKTIKIPAV 503				
Qy	367 RIWE-----SFTSGFGFT-----YTDSPOKOKKIIYRIANMISAST 424				
Db	425 VSLTYNNQTFPFIDINT--SLDPNGVRNGVSYTIVE-GPIIERSQGTNIFKG----SQK 478				
Qy	564 NVYINDKTKTLQKKFQNTVETTIEGKDLTYGSPGLEYSTTIOPPDEHPKTLTLSDLNN 623				
Db	479 GEFAIDSIIFSPV 491				
Qy	624 SFFYVDSIEFTIV 636				
RESULT 4					
AAB84630					
XX	ID AAB84630 standard; protein; 1152 AA.				
XX	AA AAB84630;				
XX	05-SEP-2001 (first entry)				
DE	Amino acid sequence of a Cry9Fa insecticidal protein.				
XX	Cry1Bf, insecticidal protein; Cry1Jd, Cry9Fa, lepidoptera; coleoptera;				
XX	insect pest; transgenic plant.				
XX	Bacillus thuringiensis.				
XX	WO200147952-A2.				
XX	05-JUL-2001.				
XX	19-DEC-2000; 2000WO-EP013184.				
XX	28-DEC-1999; 99US-0173387P.				
XX	(AVENTIS CROPS SCIENCE NV.				
PI	Arnaud G, Boets A, Damme N, Mathieu E, Vanneste S, Van Rie J;				
XX	WPI; 2001-425619/45.				
XX	DR N-PSDB; AAH28242.				
PT	Novel insecticidal proteins Cry1Jd, Cry9Fa and Cry1Bf, derived from				
XX	Bacillus thuringiensis, useful for controlling insects in plants.				
XX	Claim 11; Page 59-63; 65pp; English.				
XX	The present sequence represents Cry9Fa, an insecticidal protein derived				
CC	from Bacillus thuringiensis. The specification also describes Cry1Jd and				
CC	Cry1Jd. The Cry proteins have activity against lepidopteran and				
CC	coleopteran insect pests. Cry1Bf, Cry1Jd and Cry9Fa polynucleotides and				
CC	polypeptides are useful for obtaining a plant with resistance to insects.				
CC	Cry polynucleotides are useful for producing transgenic plants which are				
CC	resistant to insects				
XX	Sequence 1152 AA;				





DT 16-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 07-JUL-1994 (first entry)  
 XX  
 DE Bacillus thuringiensis toxin HD511.  
 XX  
 KM Bacillus thuringiensis; B.t.; Coleoptera; insect pest; toxin; HD511;  
 KM HD511; biological control agent; crystal protein; insect resistance.  
 XX  
 OS Bacillus thuringiensis; dakota.  
 XX  
 XX US5286486-A.  
 XX  
 XX 15-FEB-1994.  
 XX  
 PF 06-NOV-1992; 9AUS-00973320.  
 XX  
 PR 06-NOV-1991; 91US-00788638.  
 XX  
 XX (MYCO ) MYCOGEN CORP.  
 XX  
 PA Fu JM, Payne JM;  
 XX  
 PI N-PSDB; AA056921.  
 DR  
 DR WPI: 1994-057203/07.  
 XX  
 PT Nucleotide sequence encoding Bacillus thuringiensis toxin active against  
 PT coleopteran pests - used to produce transformed host cells with  
 PT insecticidal activity.  
 XX  
 PS Disclosure; Col 15-16 to 19-20; 16pp; English.  
 XX  
 CC Toxin HD511 (AAR46223) from B. thuringiensis dakota serotype 15 and toxin  
 CC HD867 (AAR46226) from B. thuringiensis kumamotoensis serotype 18 are  
 CC crystal proteins that can be expressed in microbial hosts for use in the  
 CC biological control of coleopteran pests, e.g. Colorado potato beetle, or  
 CC in plants to improve insect-resistance. They are encoded by sequences  
 CC AA056921-22 (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16  
 CC -OCT-2003 to standardise OS field)  
 CC  
 SQ Sequence 1138 AA;  
 Query Match 8.8%; Score 224.5; DB 2; Length 1138;  
 Best Local Similarity 22.6%; Pred. No. 9.7e-11;  
 Matches 126; Conservative 75; Mismatches 208; Indels 149; Gaps 25;  
 QY 7 TGVITQFRILNDFIKYIAKLQFTNQSDLYQPVLTLPRAQACVWHMLTKDATT--SV 64  
 DB 155 TVIDRFRLDLAFESYMSFRVA-----GYEIPLVYQAQANMLHLALRDSLTLYGDX 208  
 QY 65 WG--QOIDSQOLNGYKAEILIRILIKYTTNDVNTTNOGLELEKAKPLNDSPEEYLOAGRP 122  
 DB 209 WGFQNNLEENYNRQKMH---SESYNHCVKMYSGLS----- 243  
 QY 123 DISVRSNPKFVKMKNNKAKYKGMAMSLALFPPTGPGVPPKQALKVQSRQIPAV 182  
 DB 244 ----RLNOSTYEQWNTNRREREMTLWLDIAAFPIYDPMYMSNETSTQLRKYSDP 298  
 QY 183 IGIPIGITSQDSGPTFGSWRPDV-KTYDQIDALRLQIMELIYPLK-----SAYPW 231  
 DB 299 ISL--SISNPDIGSPSSQWMENTAFRPHVLD---YIDEIYITSKKAFAHSHIQDLFRW 353  
 QY 232 -IYESDMKRAIYVANDYIGKRGSTNGAAMHMSDPSAIYTSAL--GAAGVAPNVVGRY 288  
 DB 354 CVHAKVSFK-----KSEOSNLVTTGIYKXISGY--ISSGAY 386  
 QY 289 SHGGS--YTKGMAPA-----NTNAYAPPEPKYPGVLTGSVSAVGSK--APDADSVMF 338  
 DB 387 SRKGDLYTTLAIPSVVYPTQNTGVGEVERFVGAGH-VHYRGDKKIDVYTDSDIQLP 445  
 QY 339 GRRPVLTLENEANQLTDLALQIPAEIGITDVVPAFGRTE-----EPINGQDAIR 387  
 DB 446 DDEPI-HEKYTHRLCHATAISKSTPDYDNATIPISWTHRSAYYNNRIYNNIKIIPAVK 504

QY 388 IWE-----SFGSGPFT-----YTVDSPOKOKYKIYRIANNLSA--- 422  
 DB 505 MYKDDLDSTVYKGFQFGGLVYKRGISYIGDIAIVNSPISQKRRVAVRATSVSGLPN 564  
 QY 423 ----STVSLTYNNQTFPFDILNLTSLDPNGVYRGNGVSYTLVE-GPIIEFSQGTNFKLG-- 475  
 DB 565 VFINDIELALQNKQFQSTVETI-----GEGKDLTYGSGFYIYSTLTIOFPNHPKTLHLN 618  
 QY 476 --SQKEPAIDSIIFSPY 491  
 DB 619 HLSNNSPFYVDISIEFIPV 636  
 RESULT 7  
 AAR96126  
 ID AAR96126 standard; protein; 1169 AA.  
 XX  
 AC AAR96126;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 28-OCT-1996 (first entry)  
 XX  
 DE Bacillus thuringiensis crystal protein.  
 XX  
 KM Bacillus thuringiensis; crystal protein; delta toxin; insecticide;  
 KM lepidoptera; Coleoptera; crop protection; rice; wheat; beans; tea;  
 KM sugarcane; cauliflower; cabbage; apple; citrus fruit.  
 XX  
 OS Bacillus thuringiensis; var. japonensis.  
 OS strain N141.  
 XX  
 XX EPI711834-A2.  
 XX  
 PD 15-MAY-1996.  
 XX  
 PF 13-OCT-1995; 95EP-00307293.  
 XX  
 PR 14-OCT-1994; 94UP-00276082.  
 XX  
 PA (NISC ) NISSAN CHEM IND LTD.  
 XX  
 PI Iizuka T, Tagawa M, Arai S, Nizzekei M, Miyake T;  
 XX  
 DR WPI: 1996-232099/24. ---  
 XX  
 PT N-PSDB; AAT27148.  
 PT  
 PT B. thuringiensis var japonensis strain N141 insecticidal crystal protein  
 PT - used to protect plant from damage by pest, partic, lepidoptera or  
 PT coleoptera insects.  
 XX  
 PS Claim 3; Page 12-16; 20pp; English.  
 XX  
 CC The crystal protein is toxic to insects of the order Lepidoptera or  
 CC Coleoptera, it is therefore useful in the protection of crops which are  
 CC subject to infestation with lepidopterous or coleopterous insect pests.  
 CC The crystal protein is formulated into a spray so that the protein agent  
 CC is applied to crops at an amount of 0.1 to 5kg per hectare. Plants to be  
 CC protected by such methods include vegetables such as cauliflower and  
 CC cabbage, fruit trees such as citrus and apples, grains such as rice,  
 CC wheat and beans and industrial crops such as tea and sugarcane. (Updated  
 CC on 16-OCT-2003 to standardise OS field)  
 CC  
 SQ Sequence 1169 AA;  
 Query Match 8.7%; Score 223.5; DB 2; Length 1169;  
 Best Local Similarity 22.3%; Pred. No. 1.2e-10;  
 Matches 130; Conservative 78; Mismatches 192; Indels 183; Gaps 30;  
 QY 9 VITQFRILNDFIKYIAKLQFTNQSDLYQPVLTLPRAQACVWHMLTKDATT--SWG 66  
 DB 168 VSQFNILDSLFTQFMP--SFGSGGSGQNVATILIPVYAQANMLHLTKDADYIGARWG 225

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QY 67 QQIDSOQLNGYKAEILRLIKVYNDVNTTYNOGLELEKAKPLNYSDBEYLQAGRPDISV 126
DB 226 --LNQTOIDQFHSRQOSLTQTYTNHCVTAYNDGL-----AB 259
QY 127 LRSNFEWKKMKVAKYKRGMAASALSLAALPPTGPNYPKQALKVQSRQIFAPYIGI- 185
DB 260 LRGITTAE--SMFKYNDYRREMTLTAMDVALFPPYNLKROYPDGTNPQLTRREYTDPIAD 317
QY 186 ----PGGITSQ-----DSGPTF-GSMRFDV-----KTYDQIDALRQLMELYIQLPK 226
DB 318 PLEGP---TTQLCRSMYINPAPFRNHLNFSVLNSLRPHLPFRSLNLQILVN--YQNG 372
QY 227 SA-----YFWYTESDMKVRA--TYVNDYIGKR-----GSNTGAAWH 260
DB 373 SAMRGSRVRYHYHSSIIQEKSYGLSDPYGANINQNDIYQIISQVSNFASPVSSYS 432
QY 261 MMSDPSAIYTSN--LGAAGVAPNVGV-----RYSHGGSV 294
DB 433 VMDTN---FYLSSGVSGISGYTQGI PAVCLQQRNSTDELPSLANEGDIIIRNYSIRLSH 489
QY 295 -----TKGMAPANTNAYAPPEFYKPGYKLHSVASAYLSKAPDAADSMGFRPVLL 346
DB 490 ITQYRFQATQSGSPSTVSANLP-----TCVWTHRDVDD 523
QY 347 N--EANOQLTDTLALQIP-----AETGIDVY-PAFGRTEBPINGQDAIRIMESFTSGG 397
DB 524 NITTAQI-----TOLPLVYAYELSSGATVVKGRPF-----TGDDVIR--RTNKGGRG 569
QY 398 -FTYVYDSPQOKKYKIIYRIANNLSAS--TVSLTYNNQTFPDILNTSLDPGVGNGY 453
DB 570 AIRVASTGELTQYRIRFRYASTIIDDFVTRGCTIINFRFRYMAN-----RGQSRYE 624
QY 454 SYTLVEGPI-IEFSQGTNIFKLGSO---KGEFAIDSIIFSPV 491
DB 625 SYRTVEFTTFPNTQSDIIRTSIQGLSGNGEYVLDRIEIIPIV 667
RESULT 8
AAR46226
ID AAR46226 standard; protein; 1138 AA.
XX
AC AAR46226;
XX
DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 07-JUL-1994 (first entry)
XX
DE Bacillus thuringiensis toxin HD867.
XX
KW Bacillus thuringiensis; B.t; Coleoptera; insect pest; toxin; HD511;
KW HD867; biological control agent; crystal protein; insect resistance.
XX
OS Bacillus thuringiensis; kumamotoensis.
XX
PN US5286486-A.
XX
PD 15-FEB-1994.
XX
PF 06-NOV-1992; 92US-00973320.
XX
PR 06-NOV-1991; 91US-00788638.
XX
PA (MYCO ) MYCOGEN CORP.
XX
PI Fu JM, Payne JM;
XX
DR WPI, 1994-057203/07.
XX
DR N-PSDB; AAQ56922.
XX
PT Nucleotide sequence encoding Bacillus thuringiensis toxin active against
PT coleopteran pests - used to produce transformed host cells with
PT insecticidal activity.
XX
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PS Disclosure; Col 23-24 to 29-30; 16pp; English.
XX
XX Toxin HD511 (AAR46225) from B. thuringiensis dakota serotype 15 and toxin
CC HD867 (AAR46226) from B. thuringiensis kumamotoensis serotype 18 are
CC crystal proteins that can be expressed in microbial hosts for use in the
CC biological control of coleopteran pests, e.g. Colorado potato beetle, or
CC in plants to improve insect-resistance. They are encoded by sequences
CC AAQ56921-22. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16
CC -OCT-2003 to standardise OS field)
XX
SQ Sequence 1138 AA;
Query Match 8.7%; Score 222.5; DB 2; Length 1138;
Best Local Similarity 22.4%; Pred. No. 1.5e-10;
Matches 125; Conservative 77; Mismatches 207; Indels 149; Gaps 25;
QY 7 TGVITQPHILNDNFKYIAKLOFTNSQDLDYPUVTLPLRAQACMHMLKDATTSVWG 66
DB 155 TRVIDRFILDLFFSTMPSPRVA-----GEIPLLVYQDAANLHLALRDSI--LYG 206
QY 67 QQIDSOQLN--GYKAEILRLIKVYNDVNTTYNOGLELEKAKPLNYSDBEYLQAGRPD 123
DB 207 DKMEFTQNNIBENYNRQK-KHISEYSHNCVKYNNGLS----- 243
QY 124 ISVLRSNFEWKKMKVAKYKRGMAASALSLAALPPTGPNYPKQALKVQSRQIFAPYI 183
DB 244 ----RLNSGYEQWYNINFRREMTLTAMDVALFPIYDPNYSMETSTQLTREYTDPI 299
QY 184 GIPGIGITSODSGPTFGSM-RPDVKTYDQIDALRQLMELYIQLKSAFWYTESDMKVRA 242
DB 300 SL--SISNDGIGPSTSQMENTAIRPPLVDYDEL-----YIYSKYKAPSH 344
QY 243 YVNDYIGKRGSGNTGAAWHMS-----SDPSAIYTSAL--GAAGVAPNVGVARYSHGG 292
DB 345 RIQPLD-----FYMSAHKVSFKQSBOSNLYTGIYKGTSGYSS-----G 384
QY 293 SYT-KGMAPANTNAYAPPEFYKPGYKLHSVASAYL-----SKAPDAADV 336
DB 385 AYSFPGNDIYRTLA-APSVVYVPYQNYGVEQVEFYGVKHYDVRGDNKYLTDISTDQL 443
QY 337 MGFPRPVLLNEANQLTDTLALQIPAEIGITDVVPAPGRTE-----EPINGODA 385
DB 444 PPDGERPI-HEKYTHLCHATAISKSTPYDNATITPIFSWTHRSAAFYNRIPNKTIKPIA 502
QY 386 IRIWE-----SFTSGPFGFT-----YVDSPOKOKYKIIYRIANNLSAS 423
DB 503 YKMYKLGDTSTVVKGPFGTGLVKGSGNGYIGDIKATVNSPLSQNYRVRVYATNVSGQ 562
QY 424 TVSLTYNN-----QTFPDILNTSLDPGVGNGYSTLVE-GPIIEFSQGTNIFKLG-- 475
DB 563 --FNYSNDKITTLQRFQNTYETI--GEGKDLTYGSGFYIEYSTTTOPPDKHPIKTLHLT 618
QY 476 --SOKGEFAIDSIIFSPV 491
DB 619 DLSNNSSFYVDSIEFIPIV 636
RESULT 9
AAR37214
ID AAR37214 standard; protein; 1138 AA.
XX
AC AAR37214;
XX
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
DE B.t. toxin HD867.
XX
XX Coleopteran pests; Bacillus thuringiensis; insecticide; transgenic;
KW plant; pesticide; Colorado potato beetle.
XX
OS Bacillus thuringiensis; strain HD867.
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XX MO9108693-A1.  
 XX 13-MAY-1993.  
 XX 06-NOV-1992; 92WO-US009510.  
 XX 06-NOV-1991; 91US-00788638.  
 XX (MYCO) MYCOGEN CORP.  
 XX Payne JM, Fu JM;  
 XX WPI: 1993-167285/20.  
 XX N-PSDB; AA041745.  
 XX Control of coleopterian insect pests using bacillus thuringiensis - using  
 XX strains Bt HD 511, HD 867 or HD 1011 or their toxins or nucleotide  
 XX sequences.  
 XX Claim 10; Page 20-22; 29pp; English.  
 XX The DNA sequence encoding Bacillus thuringiensis strain HD867 toxin may  
 XX be used in an insecticide/pesticide for treatment of Coleopterian pests,  
 XX esp. the Colorado potato beetle. Strain HD867 and recombinant cells  
 XX contg. the gene encoding the toxin may be treated by chemical or physical  
 XX means to prolong the pesticidal activity of the cells, the treated cells  
 XX acting as a protective coating for the pesticidal toxin, which becomes  
 XX available upon ingestion by a target insect. The compn. may be applied  
 XX to the environment of the coleoptera, e.g. plants, soil or water, by  
 XX spraying, dusting, etc. See also AAR37214. (Updated on 25-MAR-2003 to  
 XX correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)  
 XX SQ Sequence 1138 AA;

Query Match 8.6%; Score 220.5; DB 2; Length 1138;  
 Best Local Similarity 22.5%; Pred. No. 2,3e-10;  
 Matches 124; Conservative 78; Mismatches 213; Indels 137; Gaps 24;

QY 7 TGVITQFRIANDNFYIAKLFSTNQSDLYVLTLPRAQACVHMLMLKDAFTSWG 66  
 DB 155 TVIDRFRIIDALFESYMPFRVA-----GYEIPLVYAQAAMHLALLRDS----- 203  
 QY 67 QOIDSQNGYKAEILIRIKVTVNDVNTYNOGLEEKRPINSGP-BEYIQAGRPDIS 125  
 DB 204 -----LNGDKWEFTQ-----NNIEENYNR-----QKHISEYSHCVKWNSSG----- 241  
 QY 126 VLRNPFKEVMKNNKVAKYKGMAMSALEALFPFEPVYPRQALKVQSOIFAPVIGI 185  
 DB 242 LERLNGSTYEQHINNRFRREMLIMLIDIAVFIYDPRMYSMETSTOLTREYIDPISL 301  
 QY 186 PGGITSGDSGPTFGSM-RPDVKTQIDIALRQLMELIYQPLKSAVFIYESDMKVRATV 244  
 DB 302 -SISNPGIGSPFSQMENTAIRTPHLVDYDEL-----YITSKYKAFSHSI 346  
 QY 245 NDYIGKSGNTGAAMTMS-----SPPSAYIYGAU-CAAGYAPNVVGRYSHGASY 294  
 DB 347 QPDL-----FYWSAHKVSFKOSBSQSNLYTTGIYKTSGYISS-----GAY 386  
 QY 295 T-KGMAPANTNAVAPPEFYKYP---GYKHSVSAVGL-----SKAPDAASVWF 338  
 DB 387 SERGNDIYITLA-ABSUVVYPTTONYGQVEFYGVKGVHVRGDKNDLTTSDIDLP 445  
 QY 339 GERPVLENEANQLTDTALQIPAEIGITDVVPAFGRTE-----EPINGODAIR 387  
 DB 446 DDEPI-HEKYTRHLGATATISKSTPDYDNTATIPFESWTRSAEYVNRIVPNKITIPAVK 504  
 QY 388 IWE-----SFTSGFGPT-----YVDSPOKOKYIIRINNSASAV 425  
 DB 505 MYRLGDTSTVVKPGTGDLYKRGSGNYIGDIKATVNSPLSQNKRVRVAVTVNSGQPN 564  
 QY 426 SLTVNNQTFPTDILNT-SLDPNGVRNGVSYTLVE-GPIIEFSQGTINIFKLQ-----SQKQ 479

DB 565 VYINDKITLQKRFONTVEITIGEGKDLTYGSPGYIEYSTTIQPDKHPKITLHLSLNSNS 624  
 QY 480 EFAIDSIIFSPV 491  
 DB 625 SFYVDSIEFIPV 636  
 RESULT 10  
 AAU00419  
 ID AAU00419 standard; protein, 1186 AA.  
 XX AAU00419;  
 XX 11-MAY-2001 (first entry)  
 XX DE Bacillus thuringiensis Cry1Fa/Cry1Ca (FPC1) hybrid insecticidal toxin.  
 XX Insecticidal agent; hybrid toxin; FPC1; Cry1Fa; Cry1Ca; insect control;  
 XX pest control; crop; insect resistant plant; transgenic plant;  
 XX crystal protein; mutant; mutein.  
 XX OS Bacillus thuringiensis.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 XX Domain 1..445  
 XX Region 446..454  
 XX FT /note= "Homologous crossover region (junction) between  
 XX FT domain II from Cry1Fa and domain III from Cry1Ca"  
 XX FT 455..1186  
 XX FT /note= "Domain III from Cry1Ca"  
 XX PN WO200114562-A1.  
 XX PD 01-MAR-2001.  
 XX 17-AUG-2000; 2000WO-EP008042.  
 XX PR 19-AUG-1999; 99US-00377511.  
 XX PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
 XX PI De Maagd RA, Bosch HJ, Carozzi NB, Warren GW;  
 XX DR WPI: 2001-218452/22.  
 XX N-PSDB; AA00420.  
 XX Novel hybrid insecticidal toxin useful for controlling insects such as  
 XX Spodoptera exigua and Plutella xylostella, comprises domains I and II  
 XX from Cry1F or Cry1B toxin joined to domain III from Cry1C toxin.  
 XX Claim 20; Page 77-81; 99pp; English.  
 XX The present sequence represents 1 of 3 novel hybrid insecticidal toxins  
 XX (AAU00419-AAU00423) and is designated FPC1. FPC1 comprises domains I and  
 XX II from the Cry1A toxin at the N-terminus joined to domain III from  
 XX Cry1Ca toxin at the C-terminus. In the 1186 amino acid FPC1 hybrid  
 XX sequence, the junction between the Cry1Fa and Cry1Ca toxin domains  
 XX corresponds to FPC1 residues 446-454. In the 1221 amino acid BHC13 and  
 XX BHC15 hybrid sequences, the junction between the Cry1Ba and Cry1Ca toxin  
 XX domains is residues 482-488 in the BHC13 hybrid, and residues 491-494 in  
 XX the BHC15 hybrid. The hybrid toxins are constructed by cloning and in  
 XX vivo recombination. The hybrid toxins are useful for controlling an  
 XX insect such as Spodoptera exigua (beet armyworm), Manduca sexta (tobacco  
 XX hornworm), Plutella xylostella (diamondback moth), Ostrinia nubilalis  
 XX (European corn borer), Spodoptera frugiperda (fall armyworm), and  
 XX Heliothis virescens (tobacco budworm) which are major causes of  
 XX vegetable, fruit or ornamental flower crop losses. The nucleotide  
 XX sequences encoding the hybrid toxins are useful for producing an insect-  
 XX resistant plant by introducing the nucleotide sequence into the plant  
 XX preferably a transgenic plant. The nucleotide sequences can also be  
 XX expressed in microorganisms such as a virus, bacterium and fungus and the

CC toxin produced used as an insecticidal agent. Baculoviruses engineered  
CC with the nucleotide sequence encoding a hybrid toxin can be used to  
CC infect insects in vivo resulting in their death. The hybrid toxins have a  
CC greater toxicity level than either of their parent toxins alone  
XX  
XX  
SQ Sequence 1186 AA;

Query Match 8.4%; Score 214; DB 4; Length 1186;  
Best Local Similarity 21.1%; Pred. No. 9.6e-10;  
Matches 127; Conservative 77; Mismatches 184; Indels 214; Gaps 28;

10 ITQFRIINDNFYIAKLQFSTNOSDQ-----YPL 41  
95 ITTLRLADSYEYIALRBEWENNAQLREDVRIREFANTDDALITAINFTLSFEIP 154  
42 TLPLRAQACVMHMLKDKATTSVWGQOIDSQNGYKAEILRLIKYVNDVNTYNOGHE 101  
155 LLSVYVQAANLHSLRLDAVSFGQGWGLDIATNNHNNLNLINHHYTHGCDTYNQGLE 214  
102 LEKAKPLNYSDEPEYLOAGRPDISVRSNFKYMKNNKAKYKKGAMASLSLALPPTF 161  
215 -----NLKGTWTRQ---WARFNQFRDLTLTVLDIVALFPY 248  
162 G-PNVPKQALKVQSRQIF-----APV-IGIPGITSQDSGPTFGSMRFPDKTYDQID 212  
249 DVRTPIQISSQL-TREIYTSVIEDSPVSANIPNG-----PNRAEFGVRPPLMD 298  
213 ALRQIMELYIOPLSKSAFYIYESDMKVRATYVNDYIGKRGs-----NTGAAMHMSD 265  
299 FNNSLF-VTAETVRS-----QTVMGHLVSSRNTGNRNLNPSYGVFPGALWADBD 351  
266 PSAIYTS-----ALGAAGYAPNVVVR---YSHGSGSTYKGM-----APANTN 304  
352 PPPFRTTLDPVFVRGFGNPHYVIGLRGVAFOQGTNHTRTFRNSGTTDSIDEIIPDON 411  
305 AVAPFE-----FKYPGYKLSVSAVGLSKAPDAADSVMGF--RPVLLNEANQ 351  
412 SGAPMNDYSHVNLHTFVRMPG---EISGSDSWRAP-----WFSMHRSATLTINTID- 460  
352 LITDIALQIPAEIGITDVVPAFGRTPEEPINGODAIRW--ESFTSGFGFT----- 399  
461 -----PERINQPLVKGf-----RVMGISVIITQPGFTGDIILRNMF 498  
400 -----YVVDSPQOKYKIYRIANNLASVSLT----- 428  
499 GDFVSLQVAINSPITQRYRLRFYASRDARVILVGAASGVGQVSNMPLQKTMETG 558  
429 --YNNQTF-FTDILNTSLDPNGVRNGVGYTLVEGPIIEFSQGTNIFKLGs-QXGFAID 484  
559 ENLTSRTFRYIDFSN---PFSFRANPDIIIGISEQ-----LFGAGSISGGLYID 605  
485 SI 486  
606 KI 607  
Db  
RESULT 11  
AAR54073  
ID AAR54073 standard; protein; 1167 AA.  
XX  
XX AAR54073;  
AC  
DT 02-FEB-1995 (first entry)  
XX  
XX CRYET4.  
DE  
XX  
XX CRYET4; CRYET5; Lepidoptera; Lepidopteran insect; insecticidal; toxin;  
KM insecticidal crystal protein; ICP.  
XX  
OS Bacillus thuringiensis.  
XX  
PN  
XX US5322687-A.

PD 21-JUN-1994.  
XX  
XX  
PF 29-JUL-1993; 93US-00100709.  
XX  
XX  
PR 29-JUL-1993; 93US-00100709.  
XX  
XX  
PA (ECOG-) ECOGEN INC.  
XX  
XX  
PI Tan Y, Jany CS, Donovan WP, Gonzalez JM;  
XX  
XX WPI: 1994-199503/24.  
DR N-PSDB; AA064111.  
XX

PT Isolated cryET4 gene and Bacillus thuringiensis cultures transformed with  
this gene - used in compens. against lepidopteran insects.

Claim 1; Col 15-24; 51pp; English.

CC B. thuringiensis strain EG5847 exhibits insecticidal activity against  
CC lepidopteran insects. Two novel toxin genes from B. thuringiensis EG5847  
CC designated cryET4 and cryET5 produce insecticidal proteins with activity  
CC against a broad spectrum of lepidopteran insects. The gene sequences are  
CC given in AA064111-12

SQ Sequence 1167 AA;

Query Match 8.2%; Score 210.5; DB 2; Length 1167;  
Best Local Similarity 21.9%; Pred. No. 2e-09;

Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

3 EPPSTGVITQRIINDNFYIAKLQFSTNOSDQYPLTLPLRAQACVMHMLKDKATT 62  
123 EAKSRVVIDRFRILIDGLIENAPISFRI-----IGFEVPLSVYVQAANLHLLRLDSV- 175  
63 SVWGQO--IDSQNGYKAEILRLIKYVNDVNTYNOGLEEKAKPLNYSDEPEYLOAG 120  
176 -IFGRKGLTTKNVNDYINRQIREIHEYSNHCVDITYNLE----- 215  
121 RPDISVLSNFKYMKNNKAKYKKGAMASLSLALPPTFGPN-YPRQALKVQSRQIF 179  
216 -----RLGFRSIAQWRITVNOFRRELTLTVLDIALLPND SRLYPQTSQRLREIVT 268  
180 APVIGIPGITSQDSGPTFGSMRFPDKTYDQIDALRQI---NELYIOPLSKSAFYW-- 231  
269 SPVSEFFYGVV-NSGNIIGTL---TEQOIRPRLMDFPNSMIMYSDNRREHYWGL 321  
232 ---IY-----ESDMKVRATYVND-----YIGKR 251  
322 EMTAYFTFGAQAQVSPFLVGRGSAPPLTVRSVNDGIYRILSAPFYSAPPLGTVLGSR 381  
252 GSNTGAAMHMSDDESAIYTSALGAAGYAPNVVGVRSYHSGSYTKGMAPANTNAVAPPEF 311  
382 GEKPDFALNNISPPSTIYRH---PGTVDSLVSI-----PQDNVSVF--- 421  
312 KYPGYKLSVSAVGLSKAPDAADSVMGF--RPVLLNEANQLTDTLQIPAEIGITDV 369  
422 -----HRGSHRSLSHVTMRASSPIFMTIRSATTTNTIN--FNALIQIP-----L 464  
370 VPAFRTPEPINGQAIRIMESFTSGFGFT-----YTVSPQOKYKI 412  
465 VKAFNHLH---SGATVVR-----GPGFTGDIILRTNTGTADMRVNTIGPLSQRIRV 513  
413 IYRIANNLASVSLTYNNQTFETDILNTSLDPNGVRNGVGYTLVEGPIIE----- 464  
514 RIRY-----ASTTD-----QFFTRINTSTVN---QGNF-QRTMNRDNLIESGNFRTAG 558  
465 -----FSQGNIFPLGSQ---KGFAIDSLIFSP 490  
559 FSTPFSFSAOSTFTLTGTQAFSNOEYVIDRIEFVP 593  
Db

RESULT 12  
AAR35258

ID AAW35258 standard; protein; 1167 AA.  
 XX AAW35258;  
 AC  
 XX 17-FEB-1998 (first entry)  
 DT  
 XX Bacillus thuringiensis crystal toxin CryET4.  
 DE  
 XX EG7279: crystal toxin; CryET4; lepidopteran pest; Heliothis virescens;  
 KM Helicoverpa zea; Lymantria dispar; Ostrinia nubilalis;  
 KM pseudoplusia includens; Plutella xylostella; Spodoptera exigua;  
 KM Spodoptera frugiperda; Trichoplusia ni.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 FN US679343-A.  
 EN  
 PD 21-OCT-1997.  
 XX  
 XX 07-JUN-1995; 95US-00474038.  
 PF  
 XX 29-JUL-1993; 93US-00100709.  
 PR 30-DEC-1993; 93US-00176865.  
 XX  
 PA (MONS ) MONSANTO CO.  
 XX  
 PI Jany CS, Gonzalez JM, Donovan WP, Tan Y;  
 XX  
 DR WPI, 1997-525682/48.  
 DR N-PSDB; AAT95050.  
 XX  
 XX Lepidopteran toxic Bacillus thuringiensis crystal protein - useful to  
 PT control lepidopteran pests.  
 PS  
 XX Claim 1; Col 15-24; 50pp; English.  
 CC  
 CC The present sequence is the Bacillus thuringiensis EG7279 crystal toxin  
 CC CryET4, which, optionally in association with B. thuringiensis EG7279,  
 CC can be used against lepidopteran pests. CryET4 is especially useful for  
 CC controlling Heliothis virescens, Helicoverpa zea, Lymantria dispar,  
 CC Ostrinia nubilalis, pseudoplusia includens, Plutella xylostella,  
 CC Spodoptera exigua, Spodoptera frugiperda and Trichoplusia ni.  
 CC  
 XX Sequence 1167 AA;  
 SQ  
 Query Match 8.2%; Score 210.5; DB 2; Length 1167;  
 Best Local Similarity 21.9%; Pred. No. 2e-09;  
 Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;  
 QY 3 EPPSGVITQFRILNDNFYAKLQFSTNOSDLOYPVLTPLRAQACVHMLKDAT 62  
 DB 123 EAAKSRVIDRFRILDLRANIPSPRI-----IGFEVPLLSVYQAANLHLALRDSV- 175  
 QY 63 SWMGQO-IDSOQLNGYKAEILRLIKVYNDVNTFYNOGLEKAKPLNYSDEEYLQNG 120  
 DB 176 -IFGRWGLTTXAVNDIYRQRIREIHEYSNHCVDYINTELE----- 215  
 QY 121 RPDISVLRNFKVKNVAVYKRGMAWSALSLAFTFPN-YPKQALKVOSRQIF 179  
 DB 216 -----RLGFRSIAQWRIYNOFRRLTLTVDIVALFNYSRLYPIQTSQLRREIYT 268  
 QY 180 AAVYIGPGITSDSGPTFGSMKRFVXYDQIDALRQL-----MELYIOPLSAIFW--- 231  
 DB 269 SEVSEFYGVV--NSGNIIGTL-----TEQQRRLPLMDPFNSMIMYTSNDRREHYWSGL 321  
 QY 232 ----IY-----ESDMKVRATYVND-----YIGKR 251  
 DB 322 EMTATYTGAGAGVSPVLTGTGSGAPPLTASVNDGIRIISAPYSPALGIVLGSR 381  
 QY 252 GANTGAAMWSSDPSAIYTSALGAGYAPNVVGVYRSHSGSYTKGMADANTNAYAPPEF 311  
 DB 382 GKFPDPLANNISPPSTIYRHH-----PGTVDSLVSII-----PPQNSVVP--- 421

QY 312 KYPGKLVSAVAGLSKAPPAADSVMEGF--RPVLLNENANQLLTOTALQIPAEIGITDV 369  
 DB 422 -----HRGSSHLRSHVTRKASSPIFHMTKRSATNTNTIN---PNAIIQIP-----L 464  
 QY 370 VPARGTEBPINGODAIRMESFTSGFGFT-----YTUDSPQOKYKI 412  
 DB 465 VKAFNLH-----SGATVVR-----GPGFTGGDILRRTNGTGFADMRVNTGPIUSQIRV 513  
 QY 413 IYRLANNLSASTVSLTYNNQTFPTDILNTSLDPNGVGNVGSYTLVEGPITE----- 464  
 DB 514 RIRY-----ASTTL-----OFFTRINGTSVN---QGNF-QRTMANGDNLESQNFRTAG 558  
 QY 465 -----FSQGTNIFKLGSQ--KGEPAIDSIIFSP 490  
 DB 559 FSTPFSFMAQSTFTLTGTQAFSNOGEVYIDRIEFVP 593  
 RESULT 13  
 AAM17700  
 ID AAM17700 standard; protein; 1167 AA.  
 XX  
 AC AAM17700;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-JUL-1997 (first entry)  
 XX  
 DE CryET4.  
 XX  
 XX CryET5; CryET4; Bacillus thuringiensis; insecticidal crystal protein;  
 KM ICP; toxin; CryI protein; lepidopteran insect; insecticide.  
 KM  
 OS Bacillus thuringiensis.  
 XX  
 FN US616319-A.  
 EN  
 PD 01-APR-1997.  
 XX  
 XX 30-DEC-1993; 93US-00176865.  
 PF  
 XX 29-JUL-1993; 93US-00100709.  
 PR  
 XX (MONS ) MONSANTO CO.  
 PA  
 PI Gonzalez JM, Donovan WP, Tan Y, Jany CS;  
 XX  
 DR WPI, 1997-212077/19.  
 DR N-PSDB; AAT68435.  
 XX  
 PT Bacillus thuringiensis cryET5 gene encoding insecticidal protein - useful  
 PT for control of lepidopteran pests.  
 PS  
 XX Example 3; Col 15-24; 50pp; English.  
 CC  
 CC This sequence represents the cryET4 protein of Bacillus thuringiensis  
 CC (B.t.) isolate EG5847. B.t. produces inclusions during sporulation which  
 CC include insecticidal crystal proteins (ICP). ICP toxins are active in  
 CC insects only after ingestion. Once ingested, the toxic components disrupt  
 CC the midgut cells, resulting in cessation of feeding, and eventually  
 CC death. The CryI proteins produced by B.t. are active against lepidopteran  
 CC insects. This protein, and the CryET5 protein (see AAM17699) belong to  
 CC the CryI family of ICPs. The DNA encoding this sequence can be used to  
 CC transform bacteria, which are useful as insecticides against a wide range  
 CC of lepidopteran pests, and can be applied to crops, soil and seeds. This  
 CC protein, or especially its toxic N terminal region, can be expressed in  
 CC plants, to provide protection against lepidopteran pests. The gene  
 CC encoding this sequence, or its fragments, can also be used to isolate  
 CC other similar genes. (Updated on 25-MAR-2003 to correct PF field.)  
 CC  
 XX Sequence 1167 AA;  
 SQ  
 Query Match 8.2%; Score 210.5; DB 2; Length 1167;  
 Best Local Similarity 21.9%; Pred. No. 2e-09;  
 Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;



XX Toxin; cryET4; cryET5; insecticidal; lepidoptera; transformed plant;  
KM crystal protein; insect.  
XX  
XX Bacillus thuringiensis.  
XX  
PN US5942658-A.  
XX  
PD 24-AUG-1999.  
XX  
PF 24-JUN-1997; 97US-00881340.  
XX  
PR 29-JUN-1993; 93US-00100709.  
PR 30-DEC-1993; 93US-00176865.  
PR 07-JUN-1995; 95US-00474038.  
XX  
PA (MONS ) MONSANTO CO.  
XX  
PI Gonzalez JM, Jany CS, Tan Y, Donovan WP;  
XX  
DR WPI; 1999-493544/41.  
DR N-PSDB; AA209159.  
XX  
PT Transformed plant comprising insecticidal crystal proteins.  
XX  
PS Claim 1; Fig 1A-U; 50pp; English.  
XX  
CC This invention describes novel transformed plants containing Bacillus  
CC thuringiensis strain EG5847 insecticidal crystal protein genes cryET4 or  
CC cryET5. cryET4 and cryET5 are novel toxin genes which produce  
CC insecticidal proteins with activity against a broad spectrum of insects  
CC of the order Lepidoptera. This represents the cryET4 protein described in  
CC the method of the invention  
XX  
SQ Sequence 1167 AA;  
  
Query Match 8.2%; Score 210.5; DB 2; length 1167;  
Best Local Similarity 21.9%; Pred. No. 2e-09; Matches 126; Mismatches 188; Indels 191; Gaps 26;  
Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;  
  
QY 3 EPPSTGVITQFRLINDNFIKYLAKQFSTNQSGLQVPVLTPLRAQACVMEHMLKDATY 62  
DB 123 EAKRSRVIDRFRLDGLIEANIPSPRI-----IGFEVPLSVYQANLHLALRDSV- 175  
QY 63 SVMGQ--IDSOQLNGYKAEILRLIKVYTNVNTYNOGLEKAKPLNYSDBEYLQAG 120  
DB 176 -IFGRMGILTGNVNDIYNRQIREIHEYSNHCVDFTNTELE----- 215  
QY 121 RPDISVLNSNFEKVKMKNVAKYKGMMSALSIALPFTFGPN-YPKQALKVQSRQIF 179  
DB 216 -----RLGFRSLAQWRILYNQFRELTLTLVDIALFPNYSRLYPIQFESQLTREIYT 268  
QY 180 APVIGIGGIGITSODSGPFGSMRFDVKYTDQIDALROL-----MELYIOPLKAYFW-- 231  
DB 269 SPVSEFYGVLT--NSGNITGLT-----TEQIRRHLMDFNSMIMYTSNDRREHYMSGL 321  
QY 232 ---LY-----ESDVKVRYATYVND-----YIGKR 251  
DB 322 EMTAYFTGPAQVSPPLVGTGREGSAPPLTVRSVNDGIYRILSAPFYSAPFLGITVLGSR 381  
QY 252 GSNTGAAMHMSDSDSAIYTSALGAAGYAPNVGVARYSHGSGSYTKGMAPANTNAYAPPEF 311  
DB 382 GKKFDFALNNISPPSTIYRH---PGTVDSLVS-----PPQDNSVVP--- 421  
QY 312 KYPGYKLSVSAVGLSKAPDADSVWFGF--RPVLIENANQLTDTALQIPAEIGITDV 369  
DB 422 -----HRGSSHRISHVTMRASPIFHTHRSATTNTIN--PNAIIQIP-----L 464  
QY 370 VPAFGRTPEEPINGQDAIRIMESFTSGFGFT-----YTVDSPOKQKYKI 412  
DB 465 VKAFFNLH---SGATFVR-----GPGFTGDDILARTNTGTFADMRVNITGPLSQRYRV 513  
QY 413 IYRIANNLSASTVSLTYNNQTFFTDILNLSLDPNGRGVNGVSYTLVEGPILIE----- 464

DB 514 RIRY-----ASTDL-----QFFTRINGTSYVN-----QGNF-QRTMNRGDNLGSGNFRTAG 558  
QY 465 -----FSQGTNIRKLSQ--KGEPAIDSIIFSP 490  
DB 559 FSTPFSFSMAOSTFTLGTQAFSNGQEVYIDRIEFVP 593

Search completed: October 19, 2005, 20:14:37  
Job time : 169 secs

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OM protein - protein search, using sw model

Run on: October 19, 2005, 20:08:06 ; Search time 42 Seconds

(without alignments)  
1127.111 Million cell updates/sec

Title: US-10-756-778-8  
Perfect score: 2560  
Sequence: 1 IAEPPSTVITQFRLINDNF.....KLSGQKGFALDSIFSPV 492

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	228.5	8.9	1138	2	A48944
2	207.5	8.1	1174	2	S32649
3	200	7.8	1174	2	A42459
4	199.5	7.8	1156	2	A29838
5	196	7.7	1157	1	S48247
6	194	7.6	659	2	S10228
7	186	7.3	1155	2	A26513
8	186	7.3	1155	2	JDO002
9	186	7.3	1156	2	A29125
10	184.5	7.2	1181	2	A41052
11	184	7.2	649	1	JH0261
12	184	7.2	1155	2	S02134
13	184	7.2	1155	2	I39838
14	183.5	7.2	1289	2	T18212
15	183	7.1	1385	2	T18213
16	181.5	7.1	719	2	I40590
17	177	6.9	1154	2	S39536
18	177	6.9	1160	2	S32647
19	176	6.9	1228	2	S00873
20	174	6.8	652	2	I39811
21	174	6.8	652	2	A27323
22	174	6.8	1189	2	S00944
23	172.5	6.7	1176	2	A48870
24	172	6.7	655	2	JC7140
25	169.5	6.6	719	2	I39814
26	169.5	6.6	719	2	S25383
27	169.5	6.6	1245	2	T18211
28	169	6.6	823	2	S04181
29	168.5	6.6	719	2	I39815

30	168	6.6	1136	1	USBS81	parasporal crystal
31	167.5	6.5	934	2	A22798	parasporal crystal
32	165.5	6.5	1176	2	A22617	parasporal crystal
33	165.5	6.5	1176	2	JC2219	parasporal crystal
34	165.5	6.5	1176	2	JT0241	parasporal crystal
35	165.5	6.5	1176	2	S02215	parasporal crystal
36	162	6.3	1165	2	S11446	parasporal crystal
37	160.5	6.3	934	2	B29838	parasporal crystal
38	159.5	6.2	1160	2	I40589	parasporal crystal
39	156	6.1	1177	2	A49785	parasporal crystal
40	154	6.0	618	2	S11445	parasporal crystal
41	153.5	6.0	633	2	D32053	parasporal crystal
42	151	5.9	633	2	C32053	parasporal crystal
43	151	5.9	1180	2	I39870	parasporal crystal
44	150.5	5.9	1178	1	USBSXH	parasporal crystal
45	148	5.8	1180	2	A26858	parasporal crystal

## ALIGNMENTS

```

RESULT 1
A48944
para:parasporal crystal protein cry7Aa1 - Bacillus thuringiensis
N:Alternate names: parasporal crystal protein cryIIIC
C:Species: Bacillus thuringiensis
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A48944
R:Lambert, B.; Holte, H.; Anyas, K.; Jansens, S.; Soetaert, P.; Peferoen, M.
Appl. Environ. Microbiol. 58, 2536-2542, 1992
A:Title: Novel Bacillus thuringiensis insecticidal crystal protein with a silent activit
A:Reference number: A48944; MUID:92384571; PMID:1514800
A:Contents: BT8137U
A:Accession: A48944
A:Status: Preliminary
A:Molecule type: DNA; protein
A:Residues: 1-1138 <LM>
A:Cross-references: UNIPROT:003749; GB:M64478; NID:9142760; PIDN:AAA22351.1; PID:9142761
A>Note: Sequence extracted from NCBI backbone (NCBI:112092, NCBI:P.112093)
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match      8.9%; Score 228.5; DB 2; Length 1138;
Best local similarity 22.4%; Pred. No. 9.8e-09;
Matches 124; Conservative 70; Mismatches 216; Indels 143; Gaps 23;

QY 9 VITQFRLINDNFRIKXIAKLFSTNQSDIQ-YVLTLPPLRAQACVHMLMDAT--SVW 65
DB 157 VATEFRIDSLF-----EFMSFVKYTGXEIPLVYAQAAMHLALDLSDTLYGDKW 209
QY 66 G--QQIDSQINGKAEILRLIKYITNDVNTTNOGLELEKAKPLNTSDPEEYLQAGRPD 123
DB 210 GFTQNNIEENNRK--KRISFSDHCTKYNVSGLS----- 243
QY 124 ISVLSNFKKWKNNKVAIKYKGMAMSLAALPPTGPNVPRKQALKVOSRQIFAVI 183
DB 244 ----RLNOSTYEQMNTNRRFRREMLMDLVAVPPHDPKRYSMETSTQLRVEYTPPV 299
QY 184 GIPGQITSDSGPTFGSM-RPDVKTYYDQIDALRQIMELYIOPLSAYVWYIESDMKVRAT 242
DB 300 SL--SISNPDIGSPSQMENTAIRPHLVYDDEL-----YIYSKYKAFSH 344
QY 243 YVNDYIGRGSGNTGAAMTMS-----SDPSALYTSAL--GAAGVAPNVGVGVSHGG 292
DB 345 EIQDPL-----FYWSAHKVSFKKSSQSNLYTGTIGKTSGYTSS--GAVSFGN 391
QY 293 SYTKGMAPANTVAAPFEFKYP--GYKLHVSAYGL-----SKAPDAADSVW 337
DB 392 DIYRTLA-----APSVVVPYTONYGVEQVEFGVGVGHVYRGDKNYDLTYSIDQLP 444
QY 338 FGFRPVLLNEANQLLTALQIPAEIGITDVVPAFGTE-----EPINGQDAI 386
DB 445 PDGEPI-HEKTYTHRLCHATAIFKSTPDYDNATIPFISWTHRSAEYNNRIYPNKIKIPAV 503

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Query 387 RIWE-----SFTSGFGFT-----YTVDSPQOKYKIIYRIANMLASAT 424  
Db 504 KMYKLDDBPSTVKGPGFTGDLVKRGSTGYIGDIKATVNSPLSQKRVAVRVATNVSQGF 563  
Qy 425 VSLTINNOFFFDILINT-SLDPNVGRNGNASTYLV-GEPIEFSQGTNIFKLG---SQK 478  
Db 564 NYVIDKILQTKFQWTVETIGRGKDLTYSFGYIEYSTTIOFPDEHPKITLHLSLNN 623  
Qy 479 GEPALDSIFSPY 491  
Db 624 SRFYVDISFPIV 636

RESULT 2  
S32649  
parasporal crystal protein cryIa3 - *Bacillus thuringiensis*  
C:Species: *Bacillus thuringiensis*  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S32649  
R:Lambert, B.  
submitted to the EMBL Data Library, April 1993  
A:Reference number: S32645  
A:Accession: S32649  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1174 <LAM>  
A:Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:g295865; PIDD:CAA80235.1; PID:g2958  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 8.1%; Score 207.5; DB 2; Length 1174;  
Best Local Similarity 22.7%; Pred. No. 3.9e-07;  
Matches 131; Conservative 77; Mismatches 200; Indels 169; Gaps 30;  
Qy 10 ITQFRLINDNFIKYIAKL-QFSTNQSDLQ-----YFVL 41  
Db 95 ITTLRGLADSYEYILALREWEENPNNAQLREDVRIREFANTDALLITAINNFTLSFELP 154  
Qy 42 TLPLRQAQCVMLMLLKDATTSVWGQIDSQOLNGYKALIRLIKVTNDVNTTYNGLE 101  
Db 155 LLSVYVQAANHLHLRLDAVSFGQGWGLDIATVNNHNYRLINLIRYKHCDITVNGLE 214  
Qy 102 LEKAPLWSDPEEYLQAGRPDISVLRNSFKEVMKNVAKYKRGMAASLSIALPPTF 161  
Db 215 -----NLRGNTTQ---WAFNQFRKDLTLTLVDIALVAFPNY 248  
Qy 162 GPR-YPKQALKVVSQRIF-----APV-IGIPGITSODSGPTFGSMRFDVKTVDQID 212  
Db 249 DARAYPEIQTSQQL-TREIYTSVIEDSPVSNIPNG-----FNRAEFGVRPPLMD 298  
Qy 213 ALRQIMELIYIOLPKSAVFW--IYESDMKVATVNDYIGKRGSGNTGAAMHMSDPSALY 270  
Db 299 FNNLSL-VTAETVRSQTWGHVSSRNTRAGNINPIPIYIGFNPQALIN-IADEDPRPY 356  
Qy 271 TS-----ALGAGYAPNVVGV---YSHGSGYTKGM-----APANTNAYAF 309  
Db 357 RLTSDDVFRVGRGFGNPHYVLGLRGVAPQQTGNTHTFRNSGTIDSLDEIPQDNGAWM 416  
Qy 310 E-----FKYGYKLHSVSAVGLSKAPPAADSVMGFRPVLLNEANQLLDTL 358  
Db 417 NDYSHVNLNHTVFRWPG---ELAGSDSWRAP-----MFSWTH-RSARTNININNIIT 465  
Qy 359 QIPA-----EIGITDV-VPAFGRTEBPINGODAIRMSFTSGFG-FTYVDSPQOKY 410  
Db 466 QIPAVAAHNLHSGSTVVRGPGF-----TGCDILR-RNTGTVDIRKVNITGPILSQRY 516  
Qy 411 KIIRIANMLASATVSLTYNNQTFDILINTSLDPNGVRNGSYTLVSGPIIE----- 464  
Db 517 RVRIIRY-----ASTTDL-----QFTRINGTSVN-----QGNF-QRTMNGGMLNESGNPRT 561  
Qy 465 -----FSQGTNIFKLSQKGEPAIDSIIFSP 490

Db 562 AGFTSPFSFSAQSTFTLGTQAFSNOEYVIDRIEFVP 598

RESULT 3  
A42459  
parasporal crystal protein cryIa1 - *Bacillus thuringiensis* (strain aizawai)  
N:Alternate names: parasporal crystal protein cryIF  
C:Species: *Bacillus thuringiensis*  
C>Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 09-Jul-2004  
C:Accession: A42459  
R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.  
J. Bacteriol. 173, 3966-3976, 1991  
A:Title: Isolation and characterization of a novel insecticidal crystal protein gene from  
A:Reference number: A42459; MUID:91286178; PMID:2061280  
A:Accession: A42459  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1174 <CHA>  
A:Cross-references: UNIPROT:003746; GB:M63897; NID:g142757; PIDD:AAA22348.1; PID:g142758  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 7.8%; Score 200; DB 2; Length 1174;  
Best Local Similarity 22.0%; Pred. No. 1.4e-06;  
Matches 127; Conservative 79; Mismatches 204; Indels 168; Gaps 29;  
Qy 10 ITQFRLINDNFIKYIAKL-QFSTNQSDLQ-----YFVL 41  
Db 95 ITTLRGLADSYEYILALREWEENPNNAQLREDVRIREFANTDALLITAINNFTLSFELP 154  
Qy 42 TLPLRQAQCVMLMLLKDATTSVWGQIDSQOLNGYKALIRLIKVTNDVNTTYNGLE 101  
Db 155 LLSVYVQAANHLHLRLDAVSFGQGWGLDIATVNNHNYRLINLIRYKHCDITVNGLE 214  
Qy 102 LEKAPLWSDPEEYLQAGRPDISVLRNSFKEVMKNVAKYKRGMAASLSIALPPTF 161  
Db 215 -----NLRGNTTQ---WAFNQFRKDLTLTLVDIALVAFPNY 248  
Qy 162 G-PNYPKQALKVVSQRIF-----APV-IGIPGITSODSGPTFGSMRFDVKTVDQID 212  
Db 249 DVRTYPIQTSSQL-TREIYTSVIEDSPVSNIPNG-----FNRAEFGVRPPLMD 298  
Qy 213 ALRQIMELIYIOLPKSAVFWIYESDMKVATVNDYIGKRGSG-----NTGAAMHMSD 265  
Db 299 FNNLSL-VTAETVRS-----QVWGHVSSRNTRAGNINPIPIYIGFNPQALIN-IADED 351  
Qy 266 PSAIYTS-----ALGAGYAPNVVGV---YSHGSGYTKGM-----APANTN 304  
Db 352 PRPFYRLTSDVFRVGRGFGNPHYVLGLRGVAPQQTGNTHTFRNSGTIDSLDEIPQD 411  
Qy 305 AYAPPE-----FKYGYKLHSVSAVGLSKAPPAADSVMGFRPVLLNEANQL 353  
Db 412 SGAPMNDYSHVNLNHTVFRWPG---ELSGSDSWRAP-----MFSWTH-RSARTNINID 460  
Qy 354 TDTALQIP-----AEIGITDV-VPAFGRTEBPINGODAIRMSFTSGFGFTYTV----- 402  
Db 461 PERITQIPLVKAKHTLOSQTIVVRGPGF-----TGCDILR-----RTSGCFEAYIYVIN 509  
Qy 403 -DSPQOKYKIIYRIANMLASATVSLTYNNQTFDILINTSLDPNGVRNGSY----- 455  
Db 510 GQLPQRYRARIKYSTNL---RIVYVAGRIFFGQFNKTKM-TGDDTLQOSFAYATIN 565  
Qy 456 TLVEGPPIE--FSQGTNIFKLSQKGEPAIDSIIFSP 491  
Db 566 TAFTFPMQSSFTVVGADTFSSGN---EYIDRFELIIV 600

RESULT 4  
A29838  
parasporal crystal protein - *Bacillus thuringiensis* subsp. *kurstaki*  
C:Species: *Bacillus thuringiensis* subsp. *kurstaki*  
C>Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 09-Jul-2004  
C:Accession: A29838

R:Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Wild, M.; Wallfield, A.M.  
 J. Bacteriol. 166, 801-811, 1986  
 A:Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticidal  
 A:Reference number: A84672; MUID:86223796; PMID:3011746  
 A:Accession: A29838  
 A:Molecule type: DNA  
 A:Residues: 1-1156 <THO>  
 A:Cross-references: UNIPROT:P06578; GB:M12661; NID:G143226; PIDN:AAA22613.1; PID:G143227  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 7.8%; Score 199.5; DB 2; Length 1156;  
 Best Local Similarity 21.2%; Pred. No. 1.5e-06;  
 Matches 128; Conservative 84; Mismatches 174; Indels 217; Gaps 32;

```

QY 8 GVITPRLINDNFITKIA-----KLOFTNSQDL-----QYVLTPLR 46
DB 102 GLSNLYQIYAESFRWEMADPTNPALREEMRIQFNDMSALTTAIPLFAVQNYQVPLLSVY 161
QY 47 AQACVMMHMLKDATTSVWGO--IDSQOLNGYKAEIRLIKVTNDVNTTNOGLEBK 104
DB 162 VOANMLHSVLRD--VSIFGQWGFDAATINSRYNDLTRIGNYTDHRYRMTGLE--- 216
QY 105 AKPLNYSDBEEXYQAGRDPDISVLRSNFKEVMKMKVAKYKGMASALSALPPTF-GP 163
DB 217 -----RWGPD-----SRDWIRYNGFRRELTLVLDIYSLFPNYSR 253
QY 164 NYPKQALKVQSRQIFP-VI-----GIPGGITSDSGPTGSMRFDVKTYYDQ 210
DB 254 TPIPIVSQL-TREIYTPVLENFDSFGSAQGIEGSIRSP-----HL 296
QY 211 IDALFQMLVELYIQPLKSAFMWIESDMKVRATYVNDYIGKSGSNTGAAMH--MMSDDPA 268
DB 297 MDLINSI-TIYDAHREGIYW--SGHQIMASPV---GFGSPETFPVYGTMGAAAPQ 348
QY 269 IYTSALGAAGY-----APNVGVVYSH---GQ-----SYTK----- 296
DB 349 RIVADGGGVVTRTSLTYLRPFNGINNOQLSGDGRICLMNLKKGQPYTEKAPV 408
QY 297 ---GMAFANTN-----AVAPFEFKYPGYKLSHVSAYGLSKAPDADSVMFGRPP 342
DB 409 DSPDEIPQNNNVPRQGFSHRCLAVYSWFYSGFNSVS--VIRAPV-DS----- 456
QY 343 VLEENAOQLDTALQIPAEIGIDVVPAPRGTEEPINGDAIIMESFTSGPFT--- 399
DB 457 -----SWTYSQAEFG--DVLPSSQITQIPITKIQS-WLMNSVVGKGLPFGD 500
QY 400 -----YTVDSPOKQKXIYRIANNLSASTVSLTYNNQTFPTDILNTSLDPN 446
DB 501 IIEELTQISTLRVNITAPLSQRVRRIRY-----ASTINLOP-----HTSIDR 545
QY 447 GV-RGNYSGYTLVEGPILR-----FSQGTNIFKLG---SQKGEPAIDSI 487
DB 546 PINQGNF-SATWSSGSNLQSGSFRTVGFTTPNFNSGSSVFTLSAHVFNSEVYIDRIE 604
QY 488 RSP 490
DB 605 FVP 607

```

## RESULT 5

S49247  
 parasporal crystal protein cry9Ca1 [validated] - *Bacillus thuringiensis*  
 N:Alternate names: parasporal crystal protein cry1H  
 C:Species: *Bacillus thuringiensis*  
 C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C:Accession: A59350; S49247  
 R:Lambert, B.; Buysse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinck, J.; V.  
 Appl. Environ. Microbiol. 62, 80-86, 1996  
 A:Title: A *Bacillus thuringiensis* insecticidal crystal protein with a high activity aga  
 A:Reference number: A59350; MUID:96141404; PMID:8572715  
 A:Accession: A59350  
 A:Molecule type: DNA

A:Residues: 1-1157 <LAM>  
 A:Cross-references: UNIPROT:Q45733; EMBL:Z37527; NID:9547554; PIDN:CAA85764.1; PID:95475  
 A:Experimental source: serovar colworthi  
 C:Comment: This parasporal crystal protein, active against corn borer and other insects,  
 C:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin

Query Match 7.7%; Score 196; DB 1; Length 1157;  
 Best Local Similarity 22.3%; Pred. No. 2.8e-06;  
 Matches 128; Conservative 77; Mismatches 192; Indels 178; Gaps 28;

```

QY 9 VITPRLINDNFITKIAKLOFTNSQDLQYVLTPLPRAQCVMMHMLKDATTSVWGO 68
DB 169 VRAQFALIDLPFAVAIP--LFAVNGQ--QYVPLLS--VYAQVNMHLLKLSAPFGEWG 222
QY 69 IDSQOLNGYKAEIRLIKVTNDVNTTNOGLEBKAPLAYSDBEEXYQAGRDPDISVLR 128
DB 223 FTQGEISTYDROLELAKTYNCEYTWNGDLR-----LR 258
QY 129 SNFKEVMKMKVAKYKGMASALSALPPTF-----GPYPKQALKVQSRQIFAP 181
DB 259 GTNTE--SWLRHQFRREMTLVLDVVALFPYDVRLYPTGSN--POLREYVYTDPIVNP 315
QY 182 VIGI-----PGITSDSGPTGSMRFDVKTYYDQIDALRQLM 218
DB 316 PANVGLCRMGNTPNYTFSELENAFIRPHLFDRLNSLTISNRPV----- 362
QY 219 ELIYIQPLKSAFMWIESDMKVRATYVNDYIGKRS-----NTGAAMHMSDPSAIYTA 273
DB 363 -----SSNFMWYSQHTLRYSYINDSAVQEDSYGLITTTATTINGVDGTRIESTA 414
QY 274 LGAGYAPNVVGVY--YSHGGSYTKGMAPAN-----TNAYAPFEFKYPGYKLSHVS 322
DB 415 VDFRSALIGITGVNRASVPGELFRGTTSPANGCRDLYDNDLPPD--ESTGSSTRLS 473
QY 323 -----AVGLSKAPDADSVMFGRPVL---EENAOQLDTAL-QIPAEIGITDVVA 372
DB 474 HTVFFSQTNQAGSLANA--GSVPTYVTRDVLNNTIRPNRIQLP----- 519
QY 373 FGRTEEPINGDAIRIMESFTSG-----FG-FYYTDSPOKQKXIYRIAN--N 419
DB 520 LVKASAPVSGTTVVK--GPGFTGGGILRRTTNGTGTGLRVTNVSPLTQOYRRLVRPASGN 578
QY 420 LS-----ASTVS-----LTYNQTFPTDILNTSLDPNGVNGVSGSYTLVEG 460
DB 579 FSIRVLKGVISIGVRLGSLTMMRGCELTY--ESFTRREFTTT-----GPF---N 622
QY 461 PIIERSQGTNIFKLG---SQKGEPAIDSIIFSPV 491
DB 623 PPIFTTQAGELITVNAEGVSGEYVIDRIEIVPV 657

```

## RESULT 6

S10228  
 parasporal crystal protein cry3Ba1 - *Bacillus thuringiensis* (fragment)  
 N:Alternate names: coleopterian-active parasporal crystal protein; delta-endotoxin  
 C:Species: *Bacillus thuringiensis*  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C:Accession: S10228  
 A:Status: translation not shown  
 A:Title: Nucleotide sequence of a coleopterian-active toxin gene from a new isolate of *Ba*  
 A:Reference number: S10228; MUID:90206811; PMID:2320431  
 A:Accession: S10228  
 A:Molecule type: DNA  
 A:Residues: 1-659 <STC>  
 A:Cross-references: UNIPROT:P17969; EMBL:X17123; NID:940258; PIDN:CAA34983.1; PID:940259  
 C:Genetics:  
 A:Gene: cryIIIB  
 A:Superfamily: parasporal crystal protein  
 C:Keywords: delta-endotoxin; toxin

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Query Match      7.6%; Score 194; DB 2; Length 659;
Best Local Similarity 20.2%; Pred. No. 1.7e-06;
Matches 127; Conservative 79; Mismatches 185; Indels 238; Gaps 27;

QY 1 IAEPSGTGITOPRINDNFRIKXIAKIQ-----FSTNQSLD----- 36
DB 130 IEEYAKSKALAEIQGNPFEDYVNALDSMKAPVLRSRSDRIRELPSQAEHSFRNS 189
QY 37 -----QYVLTLPRAQAQVNMHMLLDATTSSWGQO--IDSQOLNGYKAEILRLIKY 87
DB 190 MEFSAVSKFEVLFLPTFAQAANTHLLLKDA--QVGEEMGYSSEDIAEFYQQLTLTQ 247
QY 88 YTNNDVNTTNOGLELEKAPLNTSDPEYLQAGRPDIVLSRNFKVMKNTKAKYKRGK 147
DB 248 YTDHCVMNWNVGL-----NSLRGSTYDA--WVKENRRFRRM 281
QY 148 AMSALSLALPFTGPNYKQALKVQSRQIFAPVIGIGITSDSGFTSGMRPDVT 207
DB 282 TLTVLDLVLFPFYDVRLYSKGVKTELTDIFTDPIFTLAL--QYGFPTSSISNIRK 339
QY 208 YDQIDALRLQMLLYIQLKSAFYVESDMKVRATYVNDYIGKRGSTGAAMHMSDDPS 267
DB 340 PHLFDYLRGI-----EFHTRLRP--GYSGKDSFN-----YMSG-- 370
QY 268 AIYTSALGAGYAPNVGVRYSHGSGYTGMAAPANTNAAP-----EFKPYGK 317
DB 371 -----NVETRRPSIG-----SNDITLSPFGDKSIEPIQLSFDGQK 407
QY 318 LH-SVSAVGLSKAPDAADSVMEGFRPV--LLENEANOLLT-----DTAL 358
DB 408 VRTIANTDIAFPDQ--KIYGVTKVDQSQYDDQENSTQYDSCRNGYLGAQDSID 465
QY 359 QIPAEIGITD-----VVPAFGRTEEP--NGODAIRIME- 390
DB 466 QLPPE--TTDEPLEKAYSHQLNVAECFLMQDRRGITPFTMTWRSVDFTNTIDAEKITQL 523
QY 391 -----SFTSGRFT-----YTDSRP--OKOKKITYRIA 417
DB 524 PVKAYALSSGASIIIEGPGFTGNLLFLKSSNSIAKFKVTLNSALLQRYRVRIRYAST 583
QY 418 NMLASTVSLTYNNQTFFTDILNTSLDPNG-----VRGNYSYTLVEGPITERS 466
DB 584 TNL---RLFVQNSNDELVIYINKTMNTDGLTYQTFPDPAITSNMG-----FS 629
QY 467 QGTNIPLKGSQ---KGEPADISIIIFSPV 491
DB 630 GDTNDFIIGAESFVSNEKITYDKIEPIV 658

RESULT 7
para spor al crystal protein - Bacillus thuringiensis (strain aizawai)
C:Species: Bacillus thuringiensis
C:Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #ext_change 09-Jul-2004
C:Accession: A26513
R:Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H.
Gene 53, 113-119, 1987
A:Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis
A:Reference number: A26513; MUID:87248103; PMID:3297927
A:Accession: A26513
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1155 <OED>
A:Cross-references: UNIPROT:P06578; GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match      7.3%; Score 186; DB 2; Length 1155;
Best Local Similarity 20.3%; Pred. No. 1.6e-05;
Matches 122; Conservative 87; Mismatches 177; Indels 216; Gaps 30;

QY 8 GYITGFRINDNFRIKXIA-----KLOFSTNQSLD-----QYVLTLPKR 46
DB 102 GLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMSALTTALPLFAVQNYQVPLLSVY 161
QY 47 AQACVNMHMLLDKATTSWGQO--IDSQOLNGYKAEILRLIKVYTNVDVNTTNOGLELEK 104
DB 162 VQANMLHLSYLRD--VSIFGQWGMFDATINSRYNDLIRLLIGNYDHAVRWNTGLE--- 216
QY 105 AKPLNTSDPEYLQAGRPDIVLSRNFKEVMKNTKAKYKRGMAASLSLALPFTF-GP 163
DB 217 -----RWGPD-----SRDWIRYNQFRRELTLTVLDIVSLFPNYDSR 253
QY 164 NYPKQALKVQSRQIFA-PVI-----GIRGITSDSGFTSGMRPDVKTIDQ 210
DB 254 TVPIRTVQL--TRKLYTPVLENFDSFRALAQIGSIRSP-----HL 296
QY 211 IDALRLQMLLYIQLKSAFYVESDMKVRATYVNDYIGKRGSTGAAMH--MMSDDPSA 268
DB 297 MDLANSI--TIYDARGEYVW---SGHQIMASPV---GFGSPETFPFLYGTMGNAALFQ 348
QY 269 IYTSALGAGY-----APNVGV-----RSHGGS-----YTKG--- 297
DB 349 RIVAQLOGGVVKTLSSTLYRRPFNIGINNQOLSLVDGTEFAVGTSSNLPASAVYRKSGTVD 408
QY 298 ---MAPNTAYAFEEFKY-----PGYKLSVSAVGLSKAPDAADSVMEGFRFVL 344
DB 409 SLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNVS--TRAP-----MFSW--- 455
QY 345 LENEANOLLTDTALQIPAEIGITDVVPAFGRTTEEPINGODAIRIWESEFTSGRFT- 399
DB 456 -----IHSAEPNNIIPSSQITQIPLTSTMLGSGTSYVKGPGFTGIDL 500
QY 400 -----YVDSQOKOKKITYRIANNLSASTVSLYNNQTFPTDILNTSLDPNG 447
DB 501 RRTSPQISTLRVNTAQLSORVRIYR-----ASTNLQF-----HNSIDGRP 545
QY 448 V-RGVYGYTLVEGPIT-----FSQGTNIPLKGSQ---SQKGEPAIDSIIF 488
DB 546 INQGNF-SATMSSGSLQSGSFRIVGFTTPNPSGSSVFTLSAHVFNSGNEVYIDRIEF 604
QY 489 SP 490
DB 605 VP 606

RESULT 8
para spor al crystal protein cryIAb3 - Bacillus thuringiensis
N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal pro
C:Species: Bacillus thuringiensis
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #ext_change 09-Jul-2004
C:Accession: A90025; A91560; A90955; S14555; S14561; A24172; A29043; J00002
R:Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463, 1987
A:Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes fro
A:Reference number: A90025
A:Accession: A90025
A:Molecule type: mRNA
A:Residues: 1-1155 <KON>
A:Cross-references: UNIPROT:P06578
A:Experimental source: subsp. kurstaki
R:Geisler, M.; Schweitzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A:Title: The hypervariable region in the genes coding for entomopathogenic crystal prote
A:Reference number: A91560; MUID:87163505; PMID:3557124
A:Accession: A91560
A:Molecule type: DNA
A:Residues: 1-1155 <GEI>
A:Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124
A:Experimental source: subsp. kurstaki
R:Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
DNA 5, 305-314, 1986
A:Title: Bacillus thuringiensis entomocidal protoxin gene sequence and gene product anal
A:Reference number: A90955; MUID:86300092; PMID:3743328
A:Accession: A90955

```



RESULT 10  
A:1052  
parasporal crystal protein cryAe1 - Bacillus thuringiensis (strain alesti)  
C:Species: Bacillus thuringiensis  
C:Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #ext\_change 09-Jul-2004  
C:Accession: A41052  
R:Lee, C.S.; Aronson, A.I.  
J. Bacteriol. 173, 6635-6638, 1991  
A:Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subsp.  
A:Reference number: A41052; MUID:92011442; PMID:1655719  
A:Accession: A41052  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1181 <LEE>  
A:Cross-references: UNIPROT:Q03748; GB:M65252; NID:g142874; PIDN:AAA2410.1; PID:g142875  
A:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 7.2%; Score 184.5; DB 2; Length 1181;  
Best Local Similarity 20.5%; Pred. No. 2.1e-05;  
Matches 119; Conservative 87; Mismatches 191; Indels 183; Gaps 29;  
QY 2 AEPNGVITQRI-LNDNFIVIAKLQSTNOSDLQYVLTPLRAQACVHMLMKA 60  
DB 119 ADPTNPALKEEMKIQFNDMSALTATPLFTVQN--YQVPLSVYQAVNLHLSVLRD- 174  
QY 61 TTSVWGOQ--IDSQOLNGYKAEILRLIKYTVNDVNTVNOGLEKAKPLANSDEEYLD 118  
DB 175 -VSFGQGRKGLDVATINSRYNDLTRIGYTDYAAVMYNTGLE-----R 217  
QY 119 AGRPDI SVLRSNFKVKMKKAVAKYKGMASLSLALPFTF-GENYKQALKVQVSO 177  
DB 218 VNGPD-----SRDWRYNQFRRELTLTVLDIVSLFPYVDSRTYPIRTVSOQ-TRE 266  
QY 178 IPA-PVIGIPGIGTSDSGPTF-GSMRFVVKTYDQIDALRQME-----LYIQPLKSAV 229  
DB 267 ITTNPEVL-----ENFDGSPRGSQRIEQRSPHMDIINSTITTYTDAHGYY 314  
QY 230 FWIYSDMKVRATVYNDYIGKRGSTGAAMH--MMSSDPSAIYTSALGAGYA----- 280  
DB 315 YW---SGHQIMASPV---GFGSPERTFPLYGTMGAAPQQRIVAGLGGVTRTLSTTRY 367  
QY 281 --PNVGV-----RYSHGS-----YTKGMAPANTNAVAPFEKYP-----G 315  
DB 368 RNPFTIGINNORSLVDGTEFAVGSNLPASAVYRKSGTVDISLDEIPQDNNVPPRGFS 427  
QY 316 YLHSAVSAY-----GLSKAPDAADSVMEGFRVLLNEANQLTPTALQIPAEIGI 366  
DB 428 HRLSHVSMFRSGFSNSSVSIIIRAP-----MFSW-----IHRSAEF 462  
QY 367 TDVVPAGFRTSPINGQDAIRIMESFTSGFGFT-----YTVDSFOKOK 409  
DB 463 NNIISSQITQIPLRKSTNLGSGTSYVKGPGFTGDIILARTSPGQISTLRVITAPLSQR 522  
QY 410 YKIIIRIANNLSASTVSLTYNNQTFPTDILNTSLDPNGV-KNGYSYTLVSGPIIE--- 464  
DB 523 YKVRIRY-----ASTNLQF-----HTSIDRPINQCNF-SATWSSGNLQSGSF 566  
QY 465 -----FSQGTNIIFKLG-----SQKGEPAIDSIIFSP 490  
DB 567 RTVGFTTPPNFNSGSSVFTLSAHVFNSENGEVIYDRIEFVP 606

RESULT 11  
JH0261  
parasporal crystal protein cry3Ca1 - Bacillus thuringiensis subsp. kurstaki (strain B711)  
N:Alternate names: parasporal crystal protein cryIIID  
C:Species: Bacillus thuringiensis subsp. kurstaki  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #ext\_change 09-Jul-2004  
C:Accession: JH0261; S18944  
R:Lambert, B.; Theunin, W.; Aguda, R.; Van Audenhove, K.; Decock, C.; Jansens, S.; Seuri  
Gene 110, 131-132, 1992

A:Title: Nucleotide sequence of gene cryIIID encoding a novel coleopteran-active crystal  
A:Reference number: JH0261; MUID:92184108; PMID:1544571  
A:Accession: JH0261  
A:Molecule type: DNA  
A:Residues: 1-649 <LAN>  
A:Cross-references: UNIPROT:Q45744; EMBL:X59797; NID:g40287; PIDN:CAA42469.1; PID:g40288  
C:Genetics:  
A:Gene: cryIIID  
C:Superfamily: parasporal crystal protein

Query Match 7.2%; Score 184; DB 1; Length 649;  
Best Local Similarity 22.3%; Pred. No. 9.2e-06;  
Matches 122; Conservative 72; Mismatches 175; Indels 178; Gaps 30;  
QY 38 YPVLTPLPRAQACVHMLMLKDATT--SVWGOQIDSOOLNGYKAEILRLIKYTVNDVNT 95  
DB 187 YEVLPLPYQAQANHTLLLDKDAQYGDWGYSTD--DLNPFHTKQDLTLEYTHCAKW 244  
QY 96 YNQGIELEKAKPLANSDEEYLDQAGRPIDLSVLRSNFKVKMKKAVAKYKGMASLSLSLA 155  
DB 245 YKAG--LDKLGSTYEE-----WVKENRRRREMTLTVLDLI 278  
QY 156 ALFPTFGPNYKQALKVQVSOIFA-PVIGIPGIGTSDSGPTFGSMGFYKYVDQIDAL 214  
DB 279 TLPLVDRTYTKGKTELTBDVLTPIVAAN--NNNGYGTTSNIENYIRKPHLPYL 335  
QY 215 RQMLEVLIQPLKSAVFWIYSDMKVRATVYNDYIGKRGSTGAAMHMMSSDPSAIYTSAL 274  
DB 336 HAIQ--FHSRLQPGYF-----GTD--SPNYSGN--YVSTR 365  
QY 275 GAAGYAPNVGVRYSHGSGYTKGM-----APANTNAVAPFEKYPGYLHS-V 321  
DB 366 SSIG-SDEIIRSPF-YGKSTLDVQNLNFEKGVFRAVANEN-LAVWVGTVGGTGIKHSGV 422  
QY 322 SAYGSKAPDAADSVMEGFRVLLNEAN--QLTDTLQIPAEI----- 364  
DB 423 TKVQFSQYNDKDEY---RTQYDSKKNVGIVDSIDQLPITTTDSLEKAYSQNLNY 478  
QY 365 -----GITVPAFGTEEPF--NGQDAIRME-----SFTSGFGFT-- 399  
DB 479 VRCPLDGGRGIIIPFTVTHKSVDFVYNTLDESKITQIFPKAFILVNSTSVVAGGPGFTG 538  
QY 400 -----YVDSPO--KQYKIIIRIAN-----NLSASTVSLTYNNQTF 435  
DB 539 DIKCTNGSLTLVYTPAPDLTYSKYKIRIRYASTSGVRGIDIGSYTHSISYDXT-- 596  
QY 436 TDILNTSLDPNGVRN---YGSYTL--VEGPIIEFSQGTNIFKLSQSG-----EPAID 484  
DB 597 -----MD---KQNTLTNSFNLSVSVP-IEISGN--KIGSVGIGSGDEVIYID 641  
QY 485 SIIFSPV 491  
DB 642 KIEFIFM 648

RESULT 12  
S02134  
parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai ICI)  
N:Alternate names: delta-endotoxin ICI1; entomocidal crystal protein  
C:Species: Bacillus thuringiensis  
A:Variety: strain aizawai ICI  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #ext\_change 09-Jul-2004  
C:Accession: S02134; S04994  
R:Haider, M.Z.; Ellar, D.J.  
Nucleic Acids Res. 16, 10927, 1988  
A:Title: Nucleotide sequence of a Bacillus thuringiensis aizawai ICI entomocidal crystal  
A:Reference number: S02134; MUID:89083518; PMID:3205732  
A:Accession: S02134  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1155 <HAI>  
A:Cross-references: UNIPROT:P06578; EMBL:X13233; NID:g40277; PIDN:CAA31620.1; PID:g40278  
A:Experimental source: strain aizawai ICI

R:Haider, M.Z.; Ellar, D.J.  
J. Mol. Biol. 208, 183-194, 1989  
A:Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes  
A:Reference number: S04994; MUID:89362455; PMID:2769751  
A:Accession: S04994  
A:Molecule type: DNA  
A:Residues: 429-449, 'A', 451-724 <HAM>  
A:Cross-references: EMBL:X16315  
A:Experimental source: strain aizawai ICI  
C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 7.2%; Score 184; DB 2; Length 1155;  
Best Local Similarity 20.4%; Pred. No. 2.2e-05;  
Matches 121; Conservative 87; Mismatches 187; Indels 198; Gaps 29;

QY 8 GVITQFRILNDNFIXIA-----KLQFSTNSDL-----QYVLTPLR 46  
DB 102 GLSNLYQYASFRFEMADPTNPALREMRIOFNQMSALTTALPLFAVQNYQVPLLSVY 161  
QY 47 AQACVHMLMLKDATTSWGQO--IDSQQLNGYKAEILRLIKYTNVDVNTTYNGLELEK 104  
DB 162 VQANLHLSTLRD--VSFQGRMGFPAATINSRYNDLTRIGNYTDHVRWYNTGLE--- 216  
QY 105 AKPLNYSDDPEYLQAGRPDISVLRNFKEMKMKVAKYKGMMSALSIALAPPTF-GP 163  
DB 217 -----RWGPD-----SRDWIRYNQFRRELTLTVLDIVSLFPNYSR 253  
QY 164 NYPKQALKVQSRQIFA-PVI-----GIPGITSQDSGPTFGSMRFPVKTYDQ 210  
DB 254 TYPRTVSQ-LTREITNPVLENFDSFRGSAQIEGSIIRP-----HL 296  
QY 211 IDALRQLMELYIQPKSAFYWIESDKVRATYNDYIGKRGSTGAAMH--MMSDPSA 268  
DB 297 MDLINSI-TIYTDARHGEYW---SGHQIMASPV---GFGPPEFTPLYGTMGNAAPQ 348  
QY 269 IYTSALGAGY-----APNVGV-----RSHGGS-----YTKG----- 297  
DB 349 RIVAQGGVVRFTLSSTLYRRPFNIGINNQQLSVLDGTEFPAVGTSSNLSAAYRKSCTVD 408  
QY 298 ---MAPANTNAYAPFEFKYPGKLSVSAVGLSKAPDAADSVMGFRPVLLENANQL 353  
DB 409 SLDEIPPNQNNVPPROGFS-----HRLSHVSMFSGSNSVSII-IRPMS----- 454  
QY 354 TDTALQIPAEIGITDVPAFGRTTEEPINGQDAIRIWESFTSGFPT----- 399  
DB 455 ---WHRSAEFNNIIPESQITQILPKSTNLGSGTSVVKGPFTGGDILRTSPQGIS 509  
QY 400 ---YVDSPOKOKYKIIYRIANNLASASTVSLTYNNQTFPTDLINSLDPNGV-RGNYSY 455  
DB 510 TLRVNTITAPLSQRYVRIRY-----ASTNLO-----LHTSIDGRINQGNF-SA 553  
QY 456 TLVEGPILIE-----FSQGTNIFKLG-----SQKGEFAIDSIIFS 490  
DB 554 TMSGSSNLOGSFRIRVGTTPPNFSGSVFTLSAHVNGNEVYIDRIEFV 606

RESULT 13  
139838  
parasporal crystal protein - Bacillus thuringiensis

C:Species: Bacillus thuringiensis  
C>Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: 139838  
R:Hefford, M.A.; Brouseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.  
J. Biotechnol. 6, 307-322, 1987  
A:Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki  
A:Reference number: 139838  
A:Accession: 139838  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1155 <RES>  
A:Cross-references: UNIPROT:P06578; GB:M37263; NID:g142885; PIDN:AAA2420.1; PID:g142886

C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 7.2%; Score 184; DB 2; Length 1155;  
Best Local Similarity 20.1%; Pred. No. 2.2e-05;  
Matches 121; Conservative 86; Mismatches 180; Indels 214; Gaps 30;

QY 8 GVITQFRILNDNFIXIA-----KLQFSTNSDL-----QYVLTPLR 46  
DB 102 GLSNLYQYASFRFEMADPTNPALREMRIOFNQMSALTTALPLFAVQNYQVPLLSVY 161  
QY 47 AQACVHMLMLKDATTSWGQO--IDSQQLNGYKAEILRLIKYTNVDVNTTYNGLELEK 104  
DB 162 VQANLHLSTLRD--VSFQGRMGFPAATINSRYNDLTRIGNYTDHVRWYNTGLE--- 216  
QY 105 AKPLNYSDDPEYLQAGRPDISVLRNFKEMKMKVAKYKGMMSALSIALAPPTF-GP 163  
DB 217 -----RWGPD-----SRDWIRYNQFRRELTLTVLDIVSLFPNYSR 253  
QY 164 NYPKQALKVQSRQIFA-PVI-----GIPGITSQDSGPTFGSMRFPVKTYDQ 210  
DB 254 TYPRTVSQ-LTREITNPVLENFDSFRGSAQIEGSIIRP-----HL 296  
QY 211 IDALRQLMELYIQPKSAFYWIESDKVRATYNDYIGKRGSTGAAMH--MMSDPSA 268  
DB 297 MDLINSI-TIYTDARHGEYW---SGHQIMASPV---GFGPPEFTPLYGTMGNAAPQ 348  
QY 269 IYTSALGAGY-----APNVGV-----RSHGGS-----YTKG----- 297  
DB 349 RIVAQGGVVRFTLSSTLYRRPFNIGINNQQLSVLDGTEFPAVGTSSNLSAAYRKSCTVD 408  
QY 298 ---MAPANTNAYAPFEFKY-----PGKLSVSAVGLSKAPDAADSVMGFRPVL 344  
DB 409 SLDEIPPNQNNVPPROGFSHRLSHVSMFSGSNSVSII-ITAP-----MWSW----- 455  
QY 345 LENENQQLTDTALQIPAEIGITDVPAFGRTTEEPINGQDAIRIWESFTSGFPT----- 399  
DB 456 IHRAN-----FNNIIPESQITQILPKSTNLGSGTSVVKGPFTGGDIL 500  
QY 400 ---YVDSPOKOKYKIIYRIANNLASASTVSLTYNNQTFPTDLINSLDPNG 447  
DB 501 RRTSPQISTLRVNTITAPLSQRYVRIRYAST-----TLQFTTSLHGRPIN--- 547  
QY 448 VRGNVSYTLVEGPILIE-----FSQGTNIFKLG-----SQKGEFAIDSIIFS 489  
DB 548 -QGNP-SATMSSGSSNLOGSFRIRVGTTPPNFSGSVFTLSAHVNGNEVYIDRIEFV 605  
QY 490 P 490  
DB 606 P 606

RESULT 14

T18212  
parasporal crystal protein crysAb1 - Bacillus thuringiensis (fragment)

C:Species: Bacillus thuringiensis  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18212  
R:Narva, K.E.; Payne, J.M.; Schwab, G.E.; Hickie, L.A.; Galaasen, T.; Sick, A.J.  
submitted to the EMBL Data Library, July 1999  
A:Description: Novel Bacillus thuringiensis microbes active against nematodes, and genes  
A:Reference number: Z18829  
A:Accession: T18212  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1289 <NAR>  
A:Cross-references: UNIPROT:Q45753; EMBL:L07026; NID:g142769; PID:g142770; PIDN:AAA67693  
C:Genetics:  
A:Gene: CryVA(b)  
C:Keywords: delta-endotoxin

Query Match 7.2%; Score 183.5; DB 2; Length 1289;  
Best Local Similarity 20.8%; Pred. No. 2.8e-05;

	Matches	119;	Conservative	87;	Mismatches	212;	Indels	153;	Gaps	30;																																										
Qy	7	TCGVTQF	--RLINDNF	KYIAKQ	ESTNQSLQ	PLVTLPL	RAQACW	HEMLML	LDATTS	63																																										
Db	176	SGLLKFKF	DEVL	SLNSF	--YTRDL	PLVFIT	INDPAD	RTLGL	PYVALASH	HEMLML	DIITKG 234																																									
Qy	64	--WGCQID	--SQQNGY	KAELIRL	KVYTN	OVNTY	NOGLE	LELEKAP	PLANS	SDPREVLQAG 120																																										
Db	235	PTWBSKIN	FTD	DAID	SFKTD	IKNNIKL	YSKITI	YDFQGL	-----	ASyGP	----- 280																																									
Qy	121	RPDISVL	SNKE	VWKNK	VAKYK	GMAMAS	LSALALE	PTTEGP	N--YPKQA	--LKVQSRQ 177																																										
Db	281	-----	SDLESF	AKQK	YITEIM	THCH	CLDFAR	LPFP	DPDPL	YFGSGDIS	LOKTRR 329																																									
Qy	178	IFAPVIG	IRG	SITQ	DSGPT	FGSMR	FDYK	YTDQD	-----	ALRDLMELY	----- 221																																									
Db	330	ILSFPI	P----	RTAD	GLTLNT	SIDTS	NNPNY	ENGNGA	EPNPKER	ILIKQ	--FKLYPSWR 383																																									
Qy	222	-----	IQLPSA	AFWIE	SDMK	VRA	TYV-----	DYIGK	SGSTGA	AMNM--	261																																									
Db	384	AAQYGG	LLQF----	YLA	IEVD	S	VERTL	YQGL	PRAVD	QA	PNVYSID	SNPII	QIMNDT 439																																							
Qy	262	WSDPSA	LYTSAL	GA	YAPNV	-----	GVRS	--HGS	YTKG	MAPANT	NAY 306																																									
Db	440	WKTEPQ	-----	GASG	WN	TLM	RG	SVGL	SFLQ	RDGR	TL	SLA	MGCG	FADTI	YS	L	P	A	T	H	Y 492																															
Qy	307	APFERK	P-----	GK	LHS	VA	YGL	SKAP	DP	AADS	MF	FR	RV	LEN	ENQ	LL	T	T	PA	LQ	P 361																															
Db	493	LSYLYG	PIYQ	SDNS	G	HV	AL	VGS	T	POE	KL	PN	IIG	QF-----	DE	G	AN	S	T	-----	540																															
Qy	362	AEIGIT	VDVPA	F	AGRT	--E	P	INGO	DAIR	I	WES	F	T	S	G	F	T	T	V	D	S	P	KOK	K	I	I	Y	I	A	N 419																						
Db	541	--MGP	PE	FA	KA	YGG	IV	K	V	K	E	M	L	G	A	N	K	L	S	G	S	I	G	I	P	I	T	V	T	S	-----	E	Q	I	C	R	A	S	N 594													
Qy	420	LSAST	S	L	T	Y	N	N	Q	T-----	P	F	T	D	I	--L	N	T	S	L	D	P	N--G	V	R	G	N	Y	S	Y	T	L-----	V	E	G	P 461																
Db	595	--D	N	T	N	F	F	V	N	D	T	G	A	N	P	I	F	Q	O	I	N	F	A	S	T	V	N	N	T	G	V	Q	A	N	G	V	Y	V	K	S	I	A	T	D	N	S	F	T	V	K	I	P 651
Qy	462	IIF	S	O	G	N	I	F	K	L	S	Q	K	E	F	A	I	D	S	I	I	F	S	P	V 492																											
Db	652	---	A	K	T	I	V	A	L	I	N	O	G	S	D	V	F	L	D	R	I	E	F	P	I	L 678																										

RESULT 15  
T18213  
parapaporal crystal protein cry5a1 - *Bacillus thuringiensis* (fragment)  
C:Species: *Bacillus thuringiensis*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T18213  
R:Navra, K.E.; Payne, J.M.; Schwab, G.E.; Hickle, L.A.; Galasan, T.; Sick, A.J.  
submitted to the EMBL Data Library, July 1999  
A:Description: Novel *Bacillus thuringiensis* microbes active against nematodes, and genes  
A:Reference number: Z18829  
A:Accession: T18213  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1385 <NAR>  
A:Cross-references: UNIPROT:Q45760; EMBL:L07025; NID:g142868; PID:g142869; PIDN:AAA67699  
C:Genetics:  
A:Gene: CryVA (a)

[illegible]

Qy	121	RPDISVLRSNPFKMKMNWVAKYKKGMMASLSIALAEPTEGPN-YKOA--LKVQSRQ	177
Db	281	-----SDLESFAKKQKYIEIMTHHCLDPAKRLFPYTPDPLYFTSGSDISLQKTR	329
Qy	178	IFAPVIGIDGITTSDSGPFGSMKFDVKTVDQID-----ALBQMLEY--	221
Db	330	ILSPFIPi-----RTADGLTLNNTSIDTSNPNYENGGAEPNEKERILKQ-FCLYPSWR	383
Qy	222	-----IQPLKSAFYWYIESDMKRYAVN-----DYIGRKGNSNTGAAMM--	261
Db	384	AGYGGILDP-----YMAIEVODSVETRLYGQLPAVDPOAGPNVSIIDSSPIIIQIMDT	439
Qy	262	WSSDPSAITSALAGAGYAPNV-----GVRYS--HGSSYTKGMAPANTNAY	306
Db	440	WKTPPQ-----GASGMNTNLMRGSVSGSLFLODRGLRSAGKGGGADTIYSLPATHY	492
Qy	307	APPEFYKP-----GYKLSVSAIYGLSKAPDAADSVMGFRVLLLENANQLLDTALQIP	361
Db	493	LSLYVGTPTQSDNYSGHGALVGTSTQEKTLPIIG-OP-----DEQGNVST-----	540
Qy	362	AEIGIDVVPAFCRT--EEPINGOAIARIMESFTSGCFYTVVDSPOKOKYIIYRIANN	419
Db	541	--MGPFPEKASVIGIVYEMWLNGANMAKLSGQSIGIPITNVISG-----EYQIRCRASN	594
Qy	420	LSASTVSLYNNQOT-----FTTDI--LNTSLDPN-GVRGNVGSYTL-----VEGPIIEFSQ	467
Db	595	---DNTNVFENVDTGCANPIFOQINPASTVDNNTGVQAGNVYVKSIAATDNSFTEIPA	651
Qy	468	GT-NIFKLSQKGEFAIDSIISFP	490
Db	652	KTIINVAHLMQGSIDVFLDRIEFIP	675

Search completed: October 19, 2005, 20:18:30  
Job time : 44 secs

Job time : 44 secs